

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:04:02 ; Search time 19.8095 Seconds  
(without alignments)  
47.529 Million cell updates/sec

Title: US-09-776-781-6  
Perfect score: 158  
Sequence: 1 MAPSSSTKTKQLQLEHLKLMILGINNY 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	96.2	96	1	US-08-160-376A-5
2	152	96.2	96	1	US-08-389-487-8
3	152	96.2	134	6	5496924-55
4	147	93.0	50	1	US-08-127-351-13
5	147	93.0	50	1	US-08-480-367B-13
6	147	93.0	50	1	US-08-487-221A-13
7	147	93.0	50	1	US-08-480-370-13
8	147	93.0	88	4	US-08-817-787-15
9	147	93.0	133	1	US-07-800-366-1
10	147	93.0	133	1	US-08-354-456A-5
11	147	93.0	133	1	US-08-225-224-3
12	147	93.0	133	1	US-08-318-193-89
13	147	93.0	133	1	US-08-284-393B-1
14	147	93.0	133	1	US-08-284-393B-2
15	147	93.0	133	1	US-08-284-393B-3
16	147	93.0	133	1	US-08-734-471-1
17	147	93.0	133	3	US-08-722-258-3
18	147	93.0	133	4	US-08-817-787-13
19	147	93.0	133	4	US-09-310-026-1
20	147	93.0	133	5	PCT-US95-04468-3
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23	147	93.0	133	5	PCT-US95-08950-3
24	147	93.0	133	6	5210029-1
25	147	93.0	133	6	5256769-1
26	147	93.0	133	6	5464939-2
27	147	93.0	153	3	US-09-012-366-3

28 147 93.0 153 4 US-08-759-628-8  
29 147 93.0 153 4 US-09-522-217-111  
30 147 93.0 153 6 5314995-7  
31 147 93.0 157 4 US-08-818-562-2  
32 147 93.0 157 4 US-09-628-445-2  
33 147 93.0 478 3 US-08-155-888-2  
34 147 93.0 504 1 US-07-932-915-2  
35 147 93.0 504 5 PCT-US91-05826-2  
36 145 91.8 31 4 US-09-116-594-2  
37 144 91.1 251 3 US-08-875-811-59  
38 144 91.1 254 3 US-08-875-811-61  
39 143 90.5 133 1 US-08-354-456A-6  
40 132.5 83.9 127 3 US-08-806-121B-3  
41 132.5 83.9 127 4 US-09-443-061-3  
42 100 63.3 141 4 US-08-930-917A-18  
43 96 60.8 21 4 US-09-570-921-63  
44 96 60.8 21 4 US-09-570-921-68  
45 72 45.6 135 2 US-08-383-621-5

#### ALIGNMENTS

RESULT 1  
US-08-160-376A-5  
; Sequence 5, Application US/08160376A  
; Patent No. 5473049  
; GENERAL INFORMATION:  
; APPLICANT: Obermeier, Ranier  
; APPLICANT: Gerl, Martin  
; APPLICANT: Ludwig, Jurgen  
; APPLICANT: Sabel, Walter  
; TITLE OF INVENTION: Process For Obtaining Proinsulin  
; TITLE OF INVENTION: Possessing Correctly Linked  
; TITLE OF INVENTION: Cystine Bridges  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth A. Genoni, Esq.  
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500  
; CITY: Somerville  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 08876-1258  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM 386  
; OPERATING SYSTEM: WINDOWS 3.1  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/160.376A  
; FILING DATE: December 1, 1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GE P 4240420.7  
; FILING DATE: December 2, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barbara V. Maurer, Esq.  
; REGISTRATION NUMBER: 31,287  
; REFERENCE/DOCKET NUMBER: HOE 92/F 384  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 231-4079  
; TELEFAX: (908) 231-2255  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 Amino Acids  
; TYPE: Amino Acid (AA)  
; TOPOLOGY: not relevant  
; US-08-160-376A-5

Query Match 96.2%; Score 152; DB 1; Length 96;  
Best Local Similarity 96.9%; Pred. No. 4.1e-16;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



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; Sequence 13, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2554-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-367B-13

Query Match 93.0%; Score 147; DB 1; Length 5
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 1

QY 2 APTSSSTKKTQLQLEHLHLKLQMLINGNNY 32
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Db 1 APTSSSTKKTQLQLEHLHLKLQMLINGNNY 31

RESULT 6
US-08-487-221A-13
; Sequence 13, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBOLON, SPIVAK, McLELLAND, MAIER &
; ADDRESSER: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-480-370-13

Query Match 93.0%; Score 147; DB 1; Length 50;  
Best Local Similarity 96.8%; Pred. No. 1.1e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 32  
DB 1 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 31

RESULT 8  
US-08-817-787-15  
Sequence 15 Application US/08817787  
Patent No. 6294353  
GENERAL INFORMATION:  
APPLICANT: Pack, Peter  
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF  
RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,787  
FILING DATE: 23-SEP-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04117  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94 11 6558.1  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/1  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 88 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-817-787-15

Query Match 93.0%; Score 147; DB 4; Length 88;  
Best Local Similarity 96.8%; Pred. No. 2.2e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 32  
DB 1 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 31

DB 3 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 33

RESULT 9  
US-07-800-366-1  
Sequence 1 Application US/07800366  
Patent No. 5250296  
GENERAL INFORMATION:

APPLICANT: OOTSU, Koichiro  
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING  
INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/800,366  
FILING DATE: 19911127  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Castle, Donald R  
REGISTRATION NUMBER: 24,220  
REFERENCE/DOCKET NUMBER: 41417(281)  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-800-366-1

Query Match 93.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 32

DB 1 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 31

RESULT 10  
US-08-354-456A-5  
Sequence 5 Application US/08354456A  
Patent No. 5567611  
GENERAL INFORMATION:  
APPLICANT: Ralph, Peter  
APPLICANT: Martin, George  
APPLICANT: Platek, Michael  
APPLICANT: Larrick, James W.  
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: Intellectual Property - R440, P.O. Box 8097  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94662-8097

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; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/354,456A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,338
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 750.003/32387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-354-456A-5

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLKQLQMLNGINNY 32
DB 1 APTSSSTKKTQLQLEHLKQLQMLNGINNY 31

RESULT 11
US-08-225-224-3
; Sequence 3, Application US/08225224
; Patent No. 5635599
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,224
; FILING DATE: 8-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..133
; OTHER INFORMATION: /label= IL2
; US-08-225-224-3

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLKQLQMLNGINNY 32
DB 1 APTSSSTKKTQLQLEHLKQLQMLNGINNY 31

RESULT 12
US-08-318-193-89
; Sequence 89, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-193-89

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Query Match 93.0%; Score 147; DB 1; Length 133;  
 Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31

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 Job time : 20.8095 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:00:37 ; Search time 30.9841 Seconds  
(without alignments)  
137.619 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPTSSSTKTKQLQLEHLLKLQMLNGINNY 32

Scoring table: BLOSUM62

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	154	97.5	134	8	Sequence of segmen
3	153	96.8	31	23	Interleukin-2 pept
4	153	96.8	133	21	Amino acid sequenc
5	152	96.2	58	12	Human interleukin-
6	152	96.2	60	11	Human IL-2 N-termi
7	152	96.2	60	15	Human Interleukin-
8	152	96.2	96	15	Human pro-insulin
9	152	96.2	96	16	Fusion protein con
10	152	96.2	133	13	Interleukin-2 used

11	152	96.2	134	5	Sequence of an int
12	152	96.2	134	6	Sequence I of new
13	152	96.2	134	6	Sequence encoded b
14	152	96.2	134	7	Sequence of human
15	152	96.2	134	8	Sequence of mature
16	152	96.2	134	11	Sequence of natura
17	152	96.2	134	11	Sequence of natura
18	152	96.2	134	11	Human interleukin
19	152	96.2	136	20	Human interleukin
20	152	96.2	143	15	tabl. Synthetic.
21	152	96.2	149	11	Recombinant Interl
22	152	96.2	149	11	Recombinant Interl
23	152	96.2	149	11	Recombinant Interl
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25	152	96.2	149	11	Recombinant Interl
26	152	96.2	149	11	Recombinant Interl
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31	152	96.2	149	11	Recombinant Interl
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33	152	96.2	201	11	Human IL-2 N-termi
34	152	96.2	255	6	Fused antibody rec
35	152	96.2	273	6	Conjugate of inter
36	152	96.2	273	6	Interferon-gamma a
37	150	94.9	133	21	Amino acid sequenc
38	149	94.3	65	10	Human interleukin-
39	149	94.3	133	21	Amino acid sequenc
40	149	94.3	149	11	Recombinant Interl
41	149	94.3	149	11	Recombinant Interl
42	149	94.3	149	11	Recombinant Interl
43	149	94.3	149	11	Recombinant Interl
44	149	94.3	149	11	Recombinant Interl
45	149	94.3	149	11	Recombinant Interl

ALIGNMENTS

RESULT 1	
ABB79534	
ID	ABB79534 standard; Peptide; 32 AA.
AC	AC
XX	ABB79534;
XX	23-SEP-2002 (first entry)
DT	DT
XX	Interleukin-2 peptide IPI31 (D20K).
DE	IPI31; interleukin-2; human; gene; gene therapy; mutant; mutein.
KW	IPI31; interleukin-2; human; gene; gene therapy; mutant; mutein.
XX	OS
OS	Homo sapiens.
OS	Synthetic.
XX	Key
FH	Location/Qualifiers
FT	Misc-difference 21
FT	/note= *wild-type Asp substituted by Lys*
XX	US2002044935-A1.
PN	PN
XX	18-APR-2002.
PD	PD
XX	06-FEB-2001; 2001US-0776781.
XX	16-JUL-1998; 98US-0116594.
PR	12-SEP-2000; 2000US-0660465.
XX	(INSP ) INST PASTEUR.
PA	Thize J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;
XX	Mazie J;
PI	PI
XX	XX

DR WPI: 2002-546505/58.  
 DR N-PSDB; ABN84295.  
 XX New peptides derived from Interleukin 2 designated IP130 and IP131 are  
 PT useful as therapeutic agents in the treatment of patients deficient in  
 PT IL-2 activity -  
 XX  
 PS Claim 18; Page 2; 53pp; English.  
 XX  
 CC The present sequence is the protein sequence for IP131 D20K. The  
 CC sequence is based on the human Interleukin-2 (IL-2) peptide IP130  
 CC (see ABN84292) by the addition of a C-terminal Tyr residue, and  
 CC substitution of the native Asp-20 residue by Lys. Asp-20 is  
 CC located in a region of IL-2 that directly influences interaction of  
 CC the cytokine with its receptor (IL-2R). An antibody that binds to  
 CC the peptide is claimed, and is preferably an antibody produced by  
 CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting  
 CC the presence or activity of involves contacting a sample with  
 CC IP131 D20K, and detecting whether binding occurs. A claimed method  
 CC for inhibiting IL-2R activity involves contacting IL-2R with the  
 CC peptide. A claimed method for inducing IL-2 activity in a patient  
 CC comprises administering IP131 D20K to the patient. A vector  
 CC containing DNA encoding the peptide is claimed, and is used in a  
 CC claimed method for treating a patient deficient in IL-2 activity.  
 CC Also claimed are peptides corresponding to IP131 D20K but  
 CC containing conservative amino acid substitutions, i.e. change of  
 CC non-polar R-groups but other non-polar R-groups, change of  
 CC uncharged polar R-groups by other uncharged polar R-groups,  
 CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by  
 CC Gln, and vice versa. The peptide induces SHC phosphorylation or  
 CC induction of the SHC/MAPK pathway. Antibodies specific for the  
 CC peptide are useful for treatment or prevention of undesirable  
 CC immune reactions such as graft rejection, or autoimmune disorders  
 CC such as rheumatoid arthritis.  
 XX  
 SQ Sequence 32 AA;  
 Query Match 100.0%; Score 158; DB 23; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPSSSTKKTQLQLEHLLKLQMLNGINNY 32  
 DB 1 MAPSSSTKKTQLQLEHLLKLQMLNGINNY 32  
 RESULT 2  
 AAP70573  
 XX AAP70573 standard; Protein; 134 AA.  
 AC AAP70573;  
 XX  
 XX 27-MAY-1991 (first entry)  
 DT  
 XX Sequence of segments A-F of Interleukin-2 (IL-2).  
 DE  
 XX Interleukin-2 fusion protein; ballast fragment.  
 KW  
 XX Interleukin-2 fusion protein; ballast fragment.  
 PN DE3636903-A.  
 XX  
 PD 02-JUL-1987.  
 XX  
 XX 30-OCT-1986; 86DE-3636903.  
 PF  
 XX 21-DEC-1985; 85DE-3545565.  
 PR  
 PR 30-OCT-1986; 86DE-3636903.  
 XX  
 XX (FARH ) HOECHST AG.  
 PA  
 PI Habermann P;  
 XX  
 DR WPI: 1987-186353/27.  
 DR N-PSDB; AAN70921.

XX New fusion protein contg. small interleukin 2 ballast fragments -  
 PT allowing control of product solubility, and corresp. genes,  
 PT vectors and transformed host cells  
 XX  
 PS Disclosure; pp8-9; 22pp; German.  
 XX  
 CC The inventors claim a novel fusion protein which has a C- or N-  
 CC terminal portion corresponding essentially to the AA sequence of  
 CC Interleukin-2 (IL-2) but contg. less than 100 AAs. The IL-2 sequence  
 CC is coded for by 1,2 or 3 of the A-F segments of the IL-2 gene having  
 CC the formula: (EcoRI)-A-PstI-B-MluI-C-XbaI-D-SacI-E-PvuI-F-(SalI),  
 CC for example, the sequence in AAN70921. The segments are joined in any  
 CC appropriate sequence and opt. connected by usual adaptors or linkers.  
 XX  
 SQ Sequence 134 AA;  
 Query Match 97.5%; Score 154; DB 8; Length 134;  
 Best Local Similarity 96.9%; Pred. No. 4.7e-14;  
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPSSSTKKTQLQLEHLLKLQMLNGINNY 32  
 DB 1 MAPSSSTKKTQLQLEHLLKLQMLNGINNY 32  
 RESULT 3  
 ABB79535  
 ID ABB79535 standard; Peptide; 31 AA.  
 XX  
 AC ABB79535;  
 XX  
 XX 23-SEP-2002 (first entry)  
 DT  
 XX Interleukin-2 peptide IP131 (D20K).  
 DE  
 KW IP131; Interleukin-2; human; gene; gene therapy; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 20 /note= "wild-type Asp substituted by Lys"  
 FT  
 XX US2002044935-A1.  
 PN  
 XX 18-APR-2002.  
 PD  
 XX 06-FEB-2001; 2001US-0776781.  
 PF  
 XX 16-JUL-1998; 98US-0116594.  
 PR  
 PR 12-SEP-2000; 2000US-0660465.  
 XX  
 XX (INSP ) INST PASTEUR.  
 PA  
 XX Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;  
 PI Mazie J;  
 PI  
 XX WPI: 2002-546505/58.  
 DR N-PSDB; ABN84296.  
 DR  
 XX New peptides derived from Interleukin 2 designated IP130 and IP131 are  
 PT useful as therapeutic agents in the treatment of patients deficient in  
 PT IL-2 activity -  
 XX  
 PS Claim 18; Page -; 53pp; English.  
 XX  
 CC The present sequence is the protein sequence for IP131 D20K. The  
 CC sequence is based on the human Interleukin-2 (IL-2) peptide IP130  
 CC (see ABN84292) by the addition of a C-terminal Tyr residue, and  
 CC substitution of the native Asp-20 residue by Lys. Asp-20 is  
 CC located in a region of IL-2 that directly influences interaction of  
 CC the cytokine with its receptor (IL-2R). An antibody that binds to  
 CC the peptide is claimed, and is preferably an antibody produced by  
 CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting  
 CC the presence or activity of involves contacting a sample with  
 CC IP131 D20K, and detecting whether binding occurs. A claimed method  
 CC for inhibiting IL-2R activity involves contacting IL-2R with the  
 CC peptide. A claimed method for inducing IL-2 activity in a patient  
 CC comprises administering IP131 D20K to the patient. A vector  
 CC containing DNA encoding the peptide is claimed, and is used in a  
 CC claimed method for treating a patient deficient in IL-2 activity.  
 CC Also claimed are peptides corresponding to IP131 D20K but  
 CC containing conservative amino acid substitutions, i.e. change of  
 CC non-polar R-groups but other non-polar R-groups, change of  
 CC uncharged polar R-groups by other uncharged polar R-groups,  
 CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by  
 CC Gln, and vice versa. The peptide induces SHC phosphorylation or  
 CC induction of the SHC/MAPK pathway. Antibodies specific for the  
 CC peptide are useful for treatment or prevention of undesirable  
 CC immune reactions such as graft rejection, or autoimmune disorders  
 CC such as rheumatoid arthritis.



CC The sequence corresponds to the first 58 amino acid residues of  
CC human IL-2. It forms part of a fusion protein, linked to a  
CC heterologous protein. The heterologous protein is preferably gag 24  
CC or a fragment of gp 41 of HIV-1 or it is a fragment of gp 36 of  
CC HIV-2. Such fusion proteins can be used to detect antibodies to  
CC these proteins. See also AAQ10899-Q10903.

XX Sequence 58 AA;

Query Match 96.2%; Score 152; DB 12; Length 58;  
Best Local Similarity 96.9%; Pred. No. 3.6e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32  
|||||

Db 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32  
|||||

## RESULT 6

AA06838  
ID AAR06838 standard; protein; 60 AA.

XX AAR06838;

DT 14-JAN-1991 (first entry)

DE Human IL-2 N-terminal transcript of plasmid pTl3S.

KW Bovine tuberculosis; Interleukin-2; IL-2; plasmid pTl3S.

XX Mycobacterium bovis.

XX JP02195895-A.

PD 02-AUG-1990.

XX 24-JAN-1989; 89JP-0013270.

XX 24-JAN-1989; 89JP-0013270.

PA (AJIN ) AJINOMOTO KK.

XX WPI; 1990-278851/37.

DR N-PSDB; AAQ05976.

XX BCG bacteria derived immuno:protein MPB70 - can be used as  
PT diagnostic agent used to determine bovine tuberculosis.

XX Disclosure; Fig 2; 11pp; Japanese.

CC Immunoprotein MPB 70 encoding sequence may be incorporated into  
CC plasmid pTl3S with an N-terminal fragment of human IL-2. The plasmid  
CC may be used to transform an expression system giving a fusion  
CC protein which may be used as a diagnostic agent for bovine  
CC tuberculosis infection.

XX Sequence 60 AA;

Query Match 96.2%; Score 152; DB 11; Length 60;  
Best Local Similarity 96.9%; Pred. No. 3.8e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32  
|||||

Db 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32  
|||||

## RESULT 7

AA48245

ID AAR48245 standard; protein; 60 AA.

XX

AC AAR48245;

DT 12-JUL-1994 (first entry)  
XX Human Interleukin-2.  
DE  
XX  
KW non-coding region; coding region; resonance; interaction; IL-2;  
KW optimisation; degenerate sequence; plasmid pTl3Snc; pT9-11;  
KW gene expression; regulation; recombinant protein production;  
KW interleukin-2; interleukin-6.

XX Homo sapiens.

XX FR2692594-A.

XX 24-DEC-1993.

XX 22-JUN-1992; 92FR-0007571.

XX 22-JUN-1992; 92FR-0007571.

PA (PERE/) PEREZ J.

XX Perez J;

DR WPI; 1994-028256/04.

DR N-PSDB; AAQ55629; AAQ55630.

XX Application of optimised gene expression - for scientific,  
PT industrial and therapeutic purposes

XX Disclosure; Fig 28 and Fig 29; 110pp; French.

XX Resonances between coding and non-coding regions were measured for  
CC the native human IL-2 gene in plasmid pT911 (see AAQ55630) and a  
CC synthetic IL-2 gene (AAQ55629) in which alternative, degenerate  
CC codons were used in order to introduce additional restriction  
CC sites. It was found that the degenerate changes greatly upset the  
CC "natural order" between coding and non-coding regions; as a result,  
CC the amount of protein expressed by the degenerate gene is likely to  
CC be adversely affected. The inventors have proposed an "optimised"  
CC IL-2 gene with the aim of increasing the amount of protein expressed  
CC by the gene. (N.B. the sequence is also described as  
CC interleukin-6).

XX Sequence 60 AA;

Query Match 96.2%; Score 152; DB 15; Length 60;  
Best Local Similarity 96.9%; Pred. No. 3.8e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32  
|||||

Db 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32  
|||||

## RESULT 8

AA68899

ID AAR68899 standard; peptide; 96 AA.

XX AAR68899;

DT 02-MAR-1995 (first entry)

XX Human pro-insulin 2.

XX Pro-insulin; A-chain; B-chain; C-chain; disulphide;  
KW mercaptan; chaotropic agent.

XX Homo sapiens.

XX EP600372-A.

XX 08-JUN-1994.

XX

PF 25-NOV-1993; 93EP-0118993.  
 XX  
 PR 02-DEC-1992; 92DE-4240420.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Gerl M, Ludwig J, Obermeier R, Sabel W;  
 XX  
 XX WPI; 1994-177718/22.

PT Prodn. of pro-insulin with correct di-sulphide bridges - by  
 PT treating recombinant precursor protein with mercaptan in alkali  
 PT and in presence of chaotropic agent, then isolation on  
 PT hydrophobic resin  
 XX

PS Disclosure; Page 11; 15pp; German.

XX Pro-insulin is produced by treating recombinant precursor protein  
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in  
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,  
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.  
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and  
 CC desorbing the pro-insulin. This method produces pro-insulin with  
 CC correctly bonded Cys bridges. Compared with known methods it  
 CC involves fewer stages (esp. no sulphitolysis or cyanogen bromide  
 CC cleavage) and overall losses during purification are reduced, i.e.  
 CC the process is quicker and gives better yields.  
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.  
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.

XX Sequence 96 AA;

Query Match 96.2%; Score 152; DB 15; Length 96;  
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;  
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPTSSSTKTKQLQLEHLLKLQMLINGINNY 32  
 DB 1 MAPTSSSTKTKQLQLEHLLKLQMLINGINNY 32

RESULT 9

AAR78662  
 ID AAR78662 standard; protein; 96 AA.

XX AAR78662;

XX 03-APR-1996 (first entry)

XX Fusion protein contg. proinsulin sequence 3.

XX Proinsulin; post-translational modification; recombinant production;  
 KW protein folding; conformation.

XX Synthetic.

XX Key Location/Qualifiers  
 FT Region 41..44

FT /label= R2

FT /note= "a peptide of 4 amino acids"

FT Peptide 45..74

FT /label= R1-(B2-B29)-Y

FT /note= "human insulin B-chain"

FT Region 75

FT /label= X

FT Peptide 76..96

FT /label= Gly-(A2-A20)-R3

FT /note= "human insulin A-chain"

XX EP668292-A2.

XX 23-AUG-1995.

XX

PF 09-FEB-1995; 95EP-0101748.  
 XX  
 PR 18-FEB-1994; 94DE-4405179.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Gerl M, Ludwig J, Obermeier R, Sabel W;  
 XX  
 XX WPI; 1995-284754/38.

PT Isolation of insulin that is correctly post-translationally  
 PT processed - by reacting pro-insulin with a mercaptan in the presence  
 PT of a chaotropic agent and purification after absorption to hydrophobic  
 PT resin  
 XX

XX Example 2; Page 8; 16pp; German.

XX The present sequence is that of a fusion protein, produced in E.coli  
 CC which contains an example of a proinsulin molecule corresp.  
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In  
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.  
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =  
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids  
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino  
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences  
 CC from human or other insulin. The proinsulin molecule, released by  
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 SH  
 CC residues of mercaptan per Cys residue of proinsulin. The reaction  
 CC takes place in the presence of a chaotropic auxiliary agent at  
 CC pH 10-11 and results in proinsulin with correctly linked cystine  
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields  
 CC correctly folded insulin. The insulin is isolated by absorption on  
 CC a hydrophobic resin.  
 XX

SQ Sequence 96 AA;

Query Match 96.2%; Score 152; DB 16; Length 96;  
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;  
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPTSSSTKTKQLQLEHLLKLQMLINGINNY 32  
 DB 1 MAPTSSSTKTKQLQLEHLLKLQMLINGINNY 32

RESULT 10

AAR22595

ID AAR22595 standard; Protein; 133 AA.

XX AAR22595;

XX 03-NOV-1992 (first entry)

XX Interleukin-2 used to make hybrid proteins.

XX IL-2; hybrid; diphtheria; toxin; DT; proliferation; peripheral blood;  
 KW mononuclear cells; PBMC; auto-immune response; diabetes; rheumatoid;  
 KW arthritis; allograft rejection; T-suppressor.

XX Homo sapiens.

XX WO9206117-A.

XX 16-APR-1992.

XX 27-SEP-1991; 91WO-US07342.

XX 28-SEP-1990; 90US-0590113.

XX (SERA-) SERAGEN INC.

XX (UYHO-) UNIVERSITY HOSPITAL.

XX Murphy JR, Svrluga R;

XX WPI; 1992-150820/18.  
 DR N-PSDB; AAQ23867.  
 XX  
 PT Hybrid protein comprising portion of the IL-2 binding domain -  
 PT useful for inhibiting unwanted immune responses e.g. autoimmune  
 PT diseases and reaction to organ and tissue transplants  
 XX  
 PS Disclosure; Fig 1; 37pp; English.  
 XX  
 CC The interleukin-2 protein is part of a hybrid protein comprising  
 CC the binding domain of IL-2 and an enzymatically inactive fragment  
 CC of diphtheria toxin which does not include a functional DT  
 CC generalised eukaryotic binding site (see AAR26486). The hybrid  
 CC protein is capable of stimulating the proliferation of peripheral  
 CC blood mononuclear cells in vitro and of suppressing an immune  
 CC response in a mammal in vivo. The hybrid protein allows the  
 CC inhibition of an unwanted immune response such as autoimmune disease,  
 CC e.g. diabetes and rheumatoid arthritis, or allograft rejection. It  
 CC does not cause general immunosuppression, so avoids the resulting  
 CC risk of life threatening infections. In the treatment of allograft  
 CC rejection the hybrid protein spares donor-specific T-suppressor cells,  
 CC which can thus proliferate and aid in prolonging graft survival. The  
 CC hybrid protein does not need to be tailored to individual patients but  
 CC can be used as a universal inhibiting agent. Therapy need not be  
 CC continuous following allograft or an acute stage of autoimmune  
 CC disease, but can be discontinued after a course of treatment.  
 XX  
 SQ Sequence 133 AA;  
 Query Match 96.2%; Score 152; DB 13; Length 133;  
 Best Local Similarity 96.9%; Pred. No. 9e-14;  
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 MAPTSSSTKKTQLEHLLKLQMLNGINNY 32  
 DB 1 MAPTSSSTKKTQLEHLLKLQMLNGINNY 32  
 RESULT 11  
 AAP40050  
 ID AAP40050 standard; Protein; 134 AA.  
 AC AAP40050;  
 XX  
 DT 14-JAN-1992 (first entry)  
 DE  
 DE Sequence of an interleukin-2-like polypeptide encoded by the DNA  
 DE insert of pSV-hIL2-O or pSV-hIL2-1.  
 XX  
 KW Diagnosis; therapy; cancer; tumour-specific cytotoxic cell; AIDS;  
 KW multiple sclerosis; lupus; rheumatoid arthritis; herpes;  
 KW viral disease; lymphokine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP118977-A.  
 XX  
 PD 19-SEP-1984.  
 XX  
 PF 25-JAN-1984; 84EP-0300439.  
 XX  
 PR 10-JUN-1983; 83GB-0015981.  
 PR 08-FEB-1983; 83GB-0003383.  
 XX  
 PA (BIOJ ) BIOGEN NV.  
 XX  
 PI Fiers WC, Devos RR;  
 XX.  
 DR WPI; 1984-232548/38.  
 DR N-PSDB; AAN40042.  
 XX  
 PT Prodn. of human interleukin 2-like polypeptide(s) - useful

PT instead of IL-2 for stimulating the immune system etc.  
 XX  
 PS Claim 6; Page 57-58; 69pp; English.  
 XX  
 CC The DNA sequence is esp. selected from a human chromosomal gene bank,  
 CC e.g. it is a hIL-2 related portion of lamda CH4A-ghIL-2-1 or -2, or  
 CC of lamda L47-ghIL-2-1, -2 or -3. Transformed hosts are also claimed,  
 CC esp. E.coli, Ps spp., B.subtilis, B.stearothermophilus. IL-2-like  
 CC polypeptides are also claimed.  
 XX  
 SQ Sequence 134 AA;  
 Query Match 96.2%; Score 152; DB 5; Length 134;  
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;  
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 MAPTSSSTKKTQLEHLLKLQMLNGINNY 32  
 DB 1 MAPTSSSTKKTQLEHLLKLQMLNGINNY 32  
 RESULT 12  
 AAP50053  
 ID AAP50053 standard; Protein; 134 AA.  
 AC AAP50053;  
 XX  
 DT 16-AUG-2002 (updated)  
 DT 03-SEP-1991 (first entry)  
 XX  
 DE Sequence I of new biologically active interleukin 2 (IL-2).  
 XX  
 KW Immunological agent; lymphokine.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN EP163249-A.  
 XX  
 PD 04-DEC-1985.  
 XX  
 PF 28-MAY-1985; 85EP-0113324.  
 XX  
 PR 29-MAY-1984; 84DE-3419995.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Engels J, Uhlmann E, Wengenmayer F, Mullner H, Winnacker EL;  
 PI Mertz R, Okazaki H;  
 XX  
 DR WPI; 1985-304738/49.  
 DR N-PSDB; AAN50037.  
 XX  
 PT New biologically active interleukin 2 fragments and derivs. - and  
 PT coding DNA sequences, intermediate oligo-nucleotide(s), hybrid  
 PT plasmid(s) and transformed cells  
 XX  
 PS Disclosure; Page 18-20; 33pp; German.  
 XX  
 CC DNA SQs coding for AAs 1-133 and 0-133 (an additional Met) of IL-2  
 CC are claimed, including the CDS of SQ I (see AAN50037) with/without 1  
 CC or 2 stop codons. The use of a synthetic gene is esp. convenient  
 CC for expression in E. coli and allows modification of the AA SQ to  
 CC improve peptide stability, solubility or activity. The synthetic  
 CC gene was made from a series of oligonucleotides ligated to form four  
 CC larger fragments designated I1 2-I to 2-IV (see AAN50036).  
 CC (Updated on 16-AUG-2002 to add missing OS field.)  
 XX  
 SQ Sequence 134 AA;  
 Query Match 96.2%; Score 152; DB 6; Length 134;  
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;  
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
Db 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 13
AAP50855
ID AAP50855 standard; Protein; 134 AA.
XX AC AAP50855;
XX DT 03-OCT-2002 (updated)
XX DT 01-DEC-1991 (first entry)
XX DE Sequence encoded by synthetic interleukin II (IL-2) gene.
XX KW Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.
XX OS Synthetic.
XX PN WO8500817-A.
XX PD 28-FEB-1985.
XX PF 09-AUG-1984; 84WO-US01252.
XX PR 03-AUG-1984; 84US-0635941.
XX PR 10-AUG-1983; 83US-0521967.
XX PA (AMGE-) AMGEN.
XX PI Souza LM, Stabinsky Y;
XX DR WPI; 1985-062280/10.
XX DR N-PSDB; AAN50535.
XX PT Microbial expression of Interleukin II and analogues - by using
XX PT manufactured DNA sequences to transform microorganisms
XX PS Example; Table IV, Page 15-16; 39pp; English.
XX CC The inventors claim a manufactured gene for the prodn. of IL-2 and
XX CC analogues, and for polypeptides of IL-2 and analogues, and for
XX CC methods for their recombinant production.
XX CC (Updated on 03-OCT-2002 to add missing OS field.)
XX SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 6; Length 134;
Best Local Similarity 96.9%; Pred. No. 9.le-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
Db 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 14
AAP61102
ID AAP61102 standard; Protein; 134 AA.
XX AC AAP61102;
XX DT 09-MAR-1992 (first entry)
XX DE Sequence of mature human interleukin 2 (IL2) encoded by SUN-IL2.
XX KW Yeast expression vector; lymphokine.
XX OS Homo sapiens.
XX PN EP171000-A.

Query Match 96.2%; Score 152; DB 6; Length 134;
Best Local Similarity 96.9%; Pred. No. 9.le-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
Db 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 15
AAP70585
ID AAP70585 standard; protein; 134 AA.
XX AC AAP70585;
XX DT 10-APR-1991 (first entry)
XX DE Sequence of human interleukin-2 (IL-2).
XX KW Lymphokine.
XX OS Homo sapiens.
XX PN DE3541856-A.
XX PD 04-JUN-1987.
XX PF 27-NOV-1985; 85DE-3541856.
XX PR 27-NOV-1985; 85DE-3541856.
XX PA (FARH ) HOECHST AG.
XX PI Habermann P, Wengenmayer F;
XX DR WPI; 1987-157830/23.
XX DR N-PSDB; AAN70931.
XX PT Fusion proteins contg. interleukin 2 aminoacid sequences - as
XX PT well as genes coding for these proteins, vectors contg. the
XX PT genes, and host cells contg. the vectors
XX PS Example; pp 7-8; 20pp; German.
XX CC Prefd. fusion proteins are of formula Met-X-Y-Z or Met-2-Y-X. Where

```

```

XX 12-FEB-1986.
XX 26-JUL-1985; 85EP-0109405.
XX 27-JUL-1984; 84JP-0157038.
XX (SUNR ) SUNTORY LTD.
XX Oshima T, Tanaka S, Tsujimoto M, Nakazato H;
XX WPI; 1986-043554/07.
XX DR N-PSDB; AAN60198.
XX PT Protein and peptide prodn. by immobilised yeast transformant -
XX PT contg. expression vector which induces secretion of prod. from
XX PT cell into culture medium
XX PS Disclosure; Fig 6 and Page 31; 53pp; English.
XX CC The inventors claim a method for the prodn. of a substance having
XX CC the AA SQ of AAP61102. The method uses a synthetic DNA SQ (AAN60198). A
XX CC composition contg. a protein having human IL2 activity which is
XX CC produced by the method is also claimed. The method uses yeast
XX CC transformed by a secretory expression vector.
XX SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 7; Length 134;
Best Local Similarity 96.9%; Pred. No. 9.le-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
Db 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 15
AAP70585
ID AAP70585 standard; protein; 134 AA.
XX AC AAP70585;
XX DT 10-APR-1991 (first entry)
XX DE Sequence of human interleukin-2 (IL-2).
XX KW Lymphokine.
XX OS Homo sapiens.
XX PN DE3541856-A.
XX PD 04-JUN-1987.
XX PF 27-NOV-1985; 85DE-3541856.
XX PR 27-NOV-1985; 85DE-3541856.
XX PA (FARH ) HOECHST AG.
XX PI Habermann P, Wengenmayer F;
XX DR WPI; 1987-157830/23.
XX DR N-PSDB; AAN70931.
XX PT Fusion proteins contg. interleukin 2 aminoacid sequences - as
XX PT well as genes coding for these proteins, vectors contg. the
XX PT genes, and host cells contg. the vectors
XX PS Example; pp 7-8; 20pp; German.
XX CC Prefd. fusion proteins are of formula Met-X-Y-Z or Met-2-Y-X. Where

```





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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:27 ; Search time 28.9524 Seconds  
(without alignments)  
106.254 Million cell updates/sec

Title: US-09-776-781-6  
Perfect score: 158  
Sequence: 1 MAPTSSSTKKTQLEHLLKLQMLNGINNY 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR73:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	93.0	153	1	ICHU2
2	147	93.0	153	1	ICG12
3	107	67.7	154	2	JN0698
4	97	61.4	155	2	A31278
5	96	60.8	154	2	S16241
6	95	60.1	155	2	S33509
7	85	53.8	149	2	S31391
8	72	45.6	155	2	S38662
9	72	45.6	155	2	S11488
10	72	45.6	155	2	I45913
11	69	43.7	169	2	S37289
12	64	40.5	169	1	ICWS2
13	61	38.6	189	2	H64307
14	54	34.2	1061	1	GNLJG4
15	53	33.5	357	2	S12169
16	53	33.5	452	2	B84483
17	52.5	32.6	60	2	I68870
18	51.5	32.6	62	2	I54512
19	51.5	32.6	415	2	I31637
20	51	32.3	737	2	G82262
21	51	32.3	866	2	F64625
22	51	32.3	875	2	B71890
23	50.5	32.0	72	2	I68871
24	50.5	32.0	741	2	A45771
25	50	31.6	304	2	F95285
26	50	31.6	543	2	F82217
27	49.5	31.3	367	2	E84453
28	49.5	31.3	374	2	S31712
29	49	31.0	145	2	H83921

30	48.5	30.7	288	2	B89930
31	48.5	30.7	452	2	G84679
32	48	30.4	398	2	B70209
33	48	30.4	441	2	AB1367
34	48	30.4	441	2	AC1736
35	48	30.4	765	2	S76795
36	48	30.4	1964	2	AS9282
37	47.5	30.1	127	1	NRBOK2
38	47.5	30.1	244	2	T11685
39	47	29.7	257	2	S39521
40	47	29.7	307	2	T46103
41	47	29.7	406	2	S24788
42	47	29.7	432	2	S08277
43	47	29.7	511	2	D71687
44	47	29.7	531	2	T33319
45	47	29.7	564	2	S76672

ALIGNMENTS

RESULT 1

ICHU2  
Interleukin-2 precursor [validated] - human  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Homo sapiens (man)  
C:Date: 11-Aug-1983 #sequence\_revision 11-Aug-1983 #text\_change 08-Dec-2000  
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;  
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.  
Nucleic Acids Res. 12, 5005-5013, 1984  
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo  
A:Reference number: A93524; MUID:84247353; PMID:6330695  
A:Accession: A01849  
A:Molecule type: DNA  
A:Residues: 1-153 <HO2>  
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2  
R:Fujita, T.; Takooka, C.; Matsui, H.; Taniguchi, T.  
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983  
A:Title: Structure of the human interleukin 2 gene.  
A:Reference number: A21192; MUID:84170243; PMID:6324170  
A:Accession: A21192  
A:Molecule type: DNA  
A:Residues: 1-153 <FU>  
A:Cross-references: GB:J00264; NID:g186294; PIDN:AAD48509.1; PID:g5799676  
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt  
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984  
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the g  
A:Reference number: A20961; MUID:84170356; PMID:6608729  
A:Accession: A20961  
A:Molecule type: DNA  
A:Residues: 1-153 <HO2>  
A:Cross-references: GB:K02056; NID:g186302; PIDN:AAA98792.1; PID:g386819  
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi  
EMBO J. 11, 3897-3904, 1992  
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t  
A:Reference number: S31208; MUID:93010984; PMID:1396583  
A:Accession: S31209  
A:Molecule type: mRNA  
A:Residues: 11-117 <LAA>  
A:Cross-references: EMBL:Z14955  
A:Note: this sequence is shown from the beginning of the fragment to the chromosomal  
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takooka, C.; Kashima, N.; Yoshimoto, R.; Ham  
Nature 302, 305-310, 1983  
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.  
A:Reference number: A93297; MUID:83167472; PMID:6403867  
A:Accession: A93297  
A:Molecule type: mRNA  
A:Residues: 1-153 <TAN>  
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781  
A:Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC  
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K  
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983  
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840; PMID:6312994  
 A:Accession: A90113  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <MAE>  
 A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676  
 A:Experimental source: tonsillar mononuclear cells  
 R:Devos, R.; Platinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau  
 Nucleic Acids Res. 11, 4307-4323, 1983  
 A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia  
 A:Reference number: A93478; MUID:83246551; PMID:6306584  
 A:Accession: A93478  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <DEV>  
 A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781  
 A:Experimental source: splenocytes  
 R:Elzenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.  
 J. Neurochem. 64, 1928-1936, 1995  
 A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as  
 A:Reference number: I56518; MUID:95239150; PMID:7722480  
 A:Accession: I56518  
 A:Molecule type: mRNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 1-152 <EIZ>  
 A:Cross-references: GB:S77834; NID:g999000  
 A:Accession: I73624  
 A:Molecule type: mRNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 5-7,'F','9-17','P','19-32','X','34-45','X','47-143 <RES>  
 A:Cross-references: GB:S77835; NID:g999001; PIDN:AA414264.1; PID:g4261964  
 R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.  
 Biomed. Res. 6, 197-205, 1985  
 A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.  
 A:Reference number: I52528  
 A:Accession: I52528  
 A:Molecule type: DNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 1-68 <RE2>  
 A:Cross-references: GB:M33199; NID:g186296; PIDN:AAA59139.1; PID:g553508  
 R:Sleibnill, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;  
 Mol. Cell. Biol. 6, 3042-3049, 1986  
 A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and  
 A:Reference number: I57603; MUID:87064618; PMID:3491296  
 A:Accession: I57603  
 A:Molecule type: DNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 1-68 <RE3>  
 A:Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509  
 R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.  
 Biochemistry 27, 6883-6892, 1988  
 A:Title: Structure-activity relationships of recombinant human interleukin 2.  
 A:Reference number: I52401; MUID:89062420; PMID:3264184  
 A:Contents: recombinant IL-2 and mutants expressed in E. coli  
 A:Accession: I52401  
 A:Molecule type: DNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 'M', 21-153 <REA>  
 A:Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818  
 A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without  
 R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984  
 A:Title: Amino acid sequence and post-translational modification of human interleukin 2.  
 A:Reference number: A94009; MUID:85038540; PMID:6333684  
 A:Accession: A94009  
 A:Molecule type: protein  
 A:Residues: 21-153 <ROB>  
 A:Note: disulfide bonds and carbohydrate binding site were determined  
 A:Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl  
 n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)  
 R:Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.  
 J. Biol. Chem. 264, 17368-17373, 1989  
 A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and  
 de.  
 A:Reference number: A34463; MUID:90008901; PMID:2793860

A:Accession: A34463  
 A:Molecule type: protein  
 A:Residues: 21-35 <CON>  
 A:Note: the O-linked glycosylation site in recombinant material matched that from hum  
 R:Grabenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.  
 Eur. J. Biochem. 215, 189-197, 1993  
 A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro  
 A:Reference number: S34052; MUID:93345493; PMID:8344280  
 A:Contents: annotation; glycosylation of variant forms expressed in insect cells  
 C:Genetics:  
 A:Gene: GDB:IL2  
 A:Cross-references: GDB:IL9344; OMIM:147680  
 A:Map position: 4q26-4q27  
 A:Introns: 49/3; 69/3; 117/3  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-153/Product: interleukin-2 #status experimental <IL2>  
 F;23/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F;78-125/Disulfide bonds: #status experimental  
 Query Match 93.0%; Score 147; DB 1; Length 153;  
 Best Local Similarity 96.8%; Pred. No. 7.4e-14;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32  
 Db 21 APTSSSTKKTQLQLEHLLKLQMLINGINNY 51  
 RESULT 2  
 ICG12  
 Interleukin-2 precursor - common gibbon  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Hylobates lar (common gibbon, white-handed gibbon)  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
 C:Accession: A94067; A01849  
 R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985  
 A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c  
 A:Reference number: A94067; MUID:86042650; PMID:3877307  
 A:Accession: A94067  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <CHE>  
 A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015  
 A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201  
 A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-153/Product: interleukin-2 #status predicted <IL2>  
 F;23/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F;78-125/Disulfide bonds: #status predicted  
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 Best Local Similarity 96.8%; Pred. No. 7.4e-14;  
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 QY 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32  
 Db 21 APTSSSTKKTQLQLEHLLKLQMLINGINNY 51  
 RESULT 3  
 JN0698  
 Interleukin 2 precursor - cat  
 C:Species: Felis silvestris catus (domestic cat)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 16-Jul-1999  
 C:Accession: JN0698  
 R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.  
 Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993  
 A:Title: Sequence and functional characterization of feline interleukin 2.  
 A:Reference number: JN0698; MUID:93356765; PMID:8352761

A;Accession: JN0698  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-154 <COZ>  
A;Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314  
C:Superfamily: interleukin-2  
C;Keywords: growth factor

Query Match 67.7%; Score 107; DB 2; Length 154;  
Best Local Similarity 70.0%; Pred. No. 4.5e-08;  
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKKTKQLLEHLLKLQMILGINN 31  
||| ||||| ||| ||| |:::|||:  
Db 21 APASSTKETOOLEQLLDLURLLINGVNN 50

RESULT 4  
A31278  
interleukin-2 precursor - rat  
N;Alternate names: IL-2; T-cell growth factor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Apr-1989 #sequence\_revision 26-Apr-1989 #text\_change 16-Jul-1999  
C;Accession: A45882; A31278  
R;McKnight, A.J.; Mason, D.W.; Barclay, A.N.  
Immunogenetics 30, 145-147, 1989  
A;Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cfr  
A;Reference number: A45882; MUID:89339608; PMID:2788130  
A;Accession: A45882  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <MCK>  
A;Cross-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910  
C:Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 61.4%; Score 97; DB 2; Length 155;  
Best Local Similarity 64.5%; Pred. No. 1.3e-06;  
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTKQLLEHLLKLQMILGINNY 32  
|||| |::| ||| ||| |:::|||:  
Db 21 APTSSPAKETOOHLEQLLDLQVLIGIDNY 51

RESULT 5  
SI6241  
interleukin-2 precursor - pig  
N;Alternate names: IL-2; T-cell growth factor  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
C;Accession: SI6241; SI5473  
R;Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.  
Biochim. Biophys. Acta 1089, 257-258, 1991  
A;Title: cdNA cloning of porcine interleukin 2 by polymerase chain reaction.  
A;Reference number: SI6241; MUID:91274360; PMID:2054386  
A;Accession: SI6241  
A;Molecule type: mRNA  
A;Residues: 1-154 <GOO>  
A;Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992  
R;LeFebvre, F.  
submitted to the EMBL Data Library, March 1991  
A;Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain r  
A;Reference number: SI5473  
A;Accession: SI5473  
A;Molecule type: mRNA  
A;Residues: 1-154 <LEF>  
A;Cross-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069  
C:Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-154/Product: interleukin-2 #status predicted <MAT>

A;Accession: I45913  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-155 <CR>  
A;Cross-references: GB:M12791; NID:gl63204; PIDN:AAA30586.1; PID:gl63205  
R;Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.

```

RESULT 12
ICMS2
interleukin-2 precursor - mouse
N;Alternate names: IL-2; T-cell growth factor (TCGF)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-J
C;Accession: A93550; A54490; A94064; I48597; A01850; I84713
R;Fuse, A.: Fujita, T.: Yasumitsu, H.: Kashima, N.: Hasegawa, K.: TA

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C:Genetics: 33.5%; Score 53; DB 2; Length 357;  
A; Introns: 12/3; 71/1; 121/3  
C:Keywords: acyltransferase  
Query Match 33.5%; Score 53; DB 2; Length 357;  
Best Local Similarity 52.6%; Pred. No. 7.2;  
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 8 TTKTQLQLEHLLKQWIL 26  
||||| :||| || :|: :  
Db 40 TTKTQAELEQLLEQVM 58

Search completed: February 20, 2003, 10:07:24  
Job time : 30.9524 secs

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:01:02 ; Search time 7.11111 Seconds  
(without alignments)  
186.643 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPSSSTKTKTQLQLEHLLKLQMLINGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	147	93.0	153	1 IL2 HUMAN	P01585 homo sapien
2	147	93.0	154	1 IL2 MACFA	Q29615 macaca fasc
3	147	93.0	154	1 IL2 MACMU	P51498 macaca mufa
4	142	89.9	154	1 IL2 CERTO	P46649 cercopithec
5	116	73.4	154	1 IL2 MIRAN	O62641 mirounga an
6	107.5	68.0	155	1 IL2 CANFA	Q29416 canis famil
7	107	67.7	153	1 IL2 RABIT	Q77620 oryctolagus
8	107	67.7	154	1 IL2 FELCA	Q07885 felis silve
9	97	61.4	155	1 IL2 RAT	P17108 rattus norv
10	96	60.8	154	1 IL2 PIG	P26891 sus scrofa
11	95	60.1	155	1 IL2 MERUN	Q08081 meriones un
12	88	55.7	152	1 IL2 ORCOR	O97513 orcinus orc
13	85	53.8	149	1 IL2 HORSE	P37997 equus cabal
14	72	45.6	155	1 IL2 BOVIN	P05016 bos taurus
15	72	45.6	155	1 IL2 CAPHI	P36835 capra hircu
16	72	45.6	155	1 IL2 SHEEP	P19114 ovis aries
17	72	45.6	162	1 IL2 CEREL	P51747 cervus elap
18	64.5	40.8	166	1 IL2 MUSSP	Q08867 mus spretu
19	64	40.5	169	1 IL2 MOUSE	P04351 mus musculu
20	61	38.6	189	1 O64-METJA	Q60376 methanococ
21	56	35.4	1046	1 POL-SIVAG	P27980 simian immu
22	54	34.2	1061	1 POL-SIVAT	P05895 simian immu
23	53	33.5	357	1 AAAA-EMENI	P21133 emericella
24	51.5	32.6	415	1 CGA2-XENLA	P47827 xenopus lae
25	51	32.3	746	1 PCAP-HUMAN	Q96rn5 homo sapien
26	51	32.3	792	1 PCAP-MOUSE	Q924h2 mus musculu
27	50.5	32.0	741	1 RNFA-HUMAN	Q05823 homo sapien
28	48.5	30.7	452	1 TRFC-HELPI	O25867 helicobacte
29	47.5	30.1	150	1 RNK6-SAISC	O46529 saimiri sci
30	47.5	30.1	154	1 RNK6-BOVIN	P08904 bos taurus
31	47	29.7	257	1 ABCX-GALSU	P35020 galdieria s
32	47	29.7	406	1 CGA2-BOVIN	P30274 bos taurus
33	47	29.7	421	1 CGA1-MOUSE	Q61456 mus musculu

#### RESULT 1

ID	IL2_HUMAN	STANDARD;	PRT;	153 AA.
AC	P01585;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)			
DE	(Aldelesleukin).			
GN	IL2.			
OS	Homo sapiens (Human), and			
OS	Hylobates lar (Common gibbon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606; 9580;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84247353; PubMed=6330695;			
RA	Holbrook N.J., Lieber M., Crabtree G.R.;			
RT	"DNA sequence of the 5' flanking region of the human interleukin 2			
RT	gene: homologues with adult T-cell leukemia virus.";			
RL	Nucleic Acids Res. 12:5005-5013(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83167472; PubMed=6403867;			
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,			
RA	Yoshimoto R., Hamuro J.;			
RT	"Structure and expression of a cloned cDNA for human interleukin-2.";			
RL	Nature 302:305-310(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84023840; PubMed=6312994;			
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,			
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;			
RT	"Cloning of interleukin 2 mRNAs from human tonsils.";			
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83246551; PubMed=6306584;			
RA	Devos R., Platinck G., Cheroutre H., Simons G., Degraeve W.,			
RA	Tavernier J., Renaut E., Fiers W.;			
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in			
RT	E. coli.";			
RL	Nucleic Acids Res. 11:4307-4323(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84170356; PubMed=6608729;			
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,			
RA	Wiskocil R.L., Crabtree G.R.;			
RT	"T-cell growth factor: complete nucleotide sequence and organization			
RT	of the gene in normal and malignant cells.";			

P20248 homo sapien  
P78396 homo sapien  
P34408 caenorhabdi  
P26362 squalus aca  
O75148 homo sapien  
O51672 borrelia bu  
P29617 drosophila  
Q9cna0 pasteurella  
P44583 haemophilus  
P33860 saccharomyc  
P34738 neurospora  
O44218 drosophila

RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).  
RN [16]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=84170243; PubMed=6324170;  
RA Fujita T., Takaoka C., Mateui H., Taniguchi T.;  
RT "Structure of the human interleukin 2 gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).  
RN [17]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=9523150; PubMed=7722480;  
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;  
RT "Interleukin-2 transcripts in human and rodent brains: possible  
expression by astrocytes.";  
RL J. Neurochem. 64:1928-1936(1995).  
RN [18]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=96422299; PubMed=8824916;  
RA Chernicky C.L., Tan H., Burfelind P., Ilan J., Ilan J.;  
RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:  
possible role in maintenance of fetal allograft.";  
RL Mol. Reprod. Dev. 43:180-186(1996).  
RN [19]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=96422299; PubMed=8824916;  
RA Nickerson D.A.;  
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 21-153 FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=89062420; PubMed=3264184;  
RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;  
RT "Structure-activity relationships of recombinant human interleukin  
2.";  
RL Biochemistry 27:6883-6892(1988).  
RN [11]  
RP SEQUENCE OF 1-69 FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=87064618; PubMed=3491296;  
RA Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,  
R Kamoun M., Kant J.A., Crabtree G.R.;  
RT "Promoter region of interleukin-2 gene undergoes chromatin structure  
changes and confers inducibility on chloramphenicol acetyltransferase  
gene during activation of T cells.";  
RL Mol. Cell. Biol. 6:3042-3049(1986).  
RN [12]  
RP SEQUENCE OF 1-68 FROM N.A.  
RC SPECIES=Human;  
RA Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;  
RT "Organization of the DNA regions flanking the human interleukin 2  
gene.";  
RL Biomed. Res. 6:197-205(1985).  
RN [13]  
RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES=Human;  
RX MEDLINE=85038540; PubMed=6333684;  
RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;  
RT "Amino acid sequence and post-translational modification of human  
interleukin 2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).  
RN [14]  
RP CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES=Human;  
RX MEDLINE=90008901; PubMed=2793860;  
RA Conrad H.S., Nimitz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,  
R Hauser H.;  
RT "Expression of human interleukin-2 in recombinant baby hamster  
kidney, Itk-, and Chinese hamster ovary cells. Structure of O-linked  
carbohydrate chains and their location within the polypeptide.";  
RL J. Biol. Chem. 264:17368-17373(1989).

RN [15]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=86042650; PubMed=3877307;  
RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,  
R Greengard J.S., Crabtree G.R., Lin Y.;  
RT "A viral long terminal repeat in the interleukin 2 gene of a cell  
line that constitutively produces interleukin 2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RC SPECIES=Human;  
RX MEDLINE=88070646; PubMed=3500515;  
RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;  
RT "Three-dimensional structure of interleukin-2.";  
RL Science 238:1707-1709(1987).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY.  
RC SPECIES=Human;  
RX MEDLINE=92335891; PubMed=1631562;  
RA Bazan J.F.;  
RT "Unravelling the structure of IL-2.";  
RL Science 257:410-412(1992).  
RN [18]  
RP RESPONSE TO ABOVE LETTER.  
RA McKay D.B.;  
RL Science 257:412-413(1992).  
RN [19]  
RP STRUCTURE BY NMR.  
RX MEDLINE=92379010; PubMed=1510960;  
RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,  
R Campbell I.D.;  
RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR  
experiments.";  
RL Biochemistry 31:7741-7744(1992).  
RN [20]  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE=95111955; PubMed=7529123;  
RA Bamorough P., Hedgecock C.J., Richards W.G.;  
RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
modelling.";  
RL Structure 2:839-851(1994).  
RN [21]  
RP FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
RN [22]  
RP SUBCELLULAR LOCATION: Secreted.  
RN [23]  
RP DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS  
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)  
WHICH INVOLVES IL2 AND BCMA.  
RN [24]  
RP PHARMACEUTICAL: Available under the name proleukin (Chiron). Used  
in patients with renal cell carcinoma or metastatic melanoma.  
RN [25]  
RP SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
RN [26]  
RP DATABASE: NAME=R&D Systems' cytokine source book: IL2;  
WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyId=206".  
RN [27]  
RP THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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RN [28]  
RP EMBL; J00264; AAD48509.1; -  
DR EMBL; X01586; CAA25742.1; -  
DR EMBL; V00564; CAA23827.1; -  
DR EMBL; X00695; CAA25292.1; -  
DR EMBL; K02056; AAA98792.1; -  
DR EMBL; M13879; AAA59141.1; -  
DR EMBL; K03174; AAA35453.1; -  
DR EMBL; S77834; AAD14263.2; -  
DR EMBL; S82692; AAB46883.1; -



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Query Match          93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
DB  21 APTSSSTKKTQLEHLLKLQMLNGINNY 51

RESULT 2
IL2_MACFA
ID  IL2_MACFA          STANDARD;          PRT;    154 AA.
AC  Q29615;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN  IL2.
OS  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC  Cercopithecinae; Macaca.
OX  NCBI_TaxID=9541;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Peripheral blood;
RA  Yabe M., Matsuura Y., Tatsumi M.;
RL  Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC  MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC  PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC  IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC  ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC  SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D63352; BAA09676.1; -.
DR  HSSP; P01585; 3INK.
DR  InterPro: IPR000779; Interleukin-2.
DR  Pfam: PF00715; IL2; 1.
DR  PRINTS; PR00265; INTERLEUKIN2.
DR  ProDom; PD003649; Interleukin-2; 1.
DR  SMART; SM00189; IL2; 1.
DR  PROSITE; PS00424; INTERLEUKIN_2; 1.
KW  Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW  T-cell.
FT  SIGNAL. 1 20 BY SIMILARITY.
FT  CHAIN 21 154 INTERLEUKIN-2.
FT  CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
FT  DISULFID 78 126 BY SIMILARITY.
SQ  SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4A49 CRC64;

Query Match          93.0%; Score 147; DB 1; Length 154;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
DB  21 APTSSSTKKTQLEHLLKLQMLNGINNY 51

RESULT 3
IL2_MACMU
ID  IL2_MACMU          STANDARD;          PRT;    154 AA.
AC  P51498;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN  IL2.
OS  Macaca mulatta (Rhesus macaque), and
OS  Macaca nemestrina (Pig-tailed macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC  Cercopithecinae; Macaca.
OX  NCBI_TaxID=9544, 9545;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Blood;
RX  MEDLINE=96003435; PubMed=7561102;
RA  Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT  "Comparative sequence analysis of cytokine genes from human and
RT  nonhuman primates.";
RL  J. Immunol. 155:3946-3954(1995).
CC  -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC  MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC  PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC  IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC  ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC  SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC  -----
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CC  -----
DR  EMBL; U19847; AAB60400.1; -.
DR  EMBL; U19852; AAA86714.1; -.
DR  HSSP; P01585; 3INK.
DR  InterPro: IPR000779; Interleukin-2.
DR  Pfam: PF00715; IL2; 1.
DR  PRINTS; PR00265; INTERLEUKIN2.
DR  ProDom; PD003649; Interleukin-2; 1.
DR  SMART; SM00189; IL2; 1.
DR  PROSITE; PS00424; INTERLEUKIN_2; 1.
KW  Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW  T-cell.
FT  SIGNAL. 1 20 BY SIMILARITY.
FT  CHAIN 21 154 INTERLEUKIN-2.
FT  CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
FT  DISULFID 78 126 BY SIMILARITY.
SQ  SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match          93.0%; Score 147; DB 1; Length 154;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
DB  21 APTSSSTKKTQLEHLLKLQMLNGINNY 51

RESULT 4
IL2_CERTO
ID  IL2_CERTO          STANDARD;          PRT;    154 AA.
AC  P46649;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN  IL2.
```







CC	
DR	EMBL; X68779; CAA48679.1; -.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 >152 INTERLEUKIN-2.  
 FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.  
 FT NON\_TER 152 152  
 SQ SEQUENCE 152 AA; 17424 MW; 308F91821ECCB764 CRC64;

Query Match 55.7%; Score 88; DB 1; Length 152;  
 Best Local Similarity 58.1%; Pred. No. 4.1e-06;  
 Matches 18; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32  
 ||||| : : : : :  
 Db 21 APTSSSTNTKQVSLQQLQLLLKEINNY 51

## RESULT 13

IL2\_HORSE STANDARD; PRT; 149 AA.  
 ID IL2\_HORSE  
 AC P37997;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94160538; PubMed=8116217;  
 RA Vandergriff E.V., Horohov D.W.;  
 RT "Molecular cloning and expression of equine interleukin 2.";  
 RL Vet. Immunol. Immunopathol. 39:395-406(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tavernor A.S., Allen W.R., Butcher G.W.;  
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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 CC  
 CC EMBL; L06009; AAA20134.1; -  
 CC EMBL; X69393; CAA49190.1; -  
 CC PIR; S31391; S31391.  
 CC HSP; P01585; 3INK.  
 CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam; PF00715; IL2; 1.  
 CC PRINTS; PR00265; INTERLEUKIN2.  
 CC PRODOM; PD003649; Interleukin-2; 1.  
 CC SMART; SM00189; IL2; 1.  
 CC PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 CC T-cell.  
 KW SIGNAL 1 20 BY SIMILARITY.  
 KW CHAIN 21 149 INTERLEUKIN-2.  
 FT FT DISULFID 78 121 BY SIMILARITY.  
 FT FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT FT CARBOHYD 106 106 N-LINKED (GLCNA. . .) (POTENTIAL).  
 FT FT CONFLICT 3 3 R -> K (IN REF. 2).

FT CONFLICT 8 8 S -> A (IN REF. 2).  
 FT CONFLICT 59 59 I -> M (IN REF. 2).  
 FT CONFLICT 125 125 N -> D (IN REF. 2).  
 FT CONFLICT 128 128 E -> G (IN REF. 2).  
 FT CONFLICT 145 145 I -> F (IN REF. 2).  
 FT CONFLICT 148 148 L -> M (IN REF. 2).  
 SQ SEQUENCE 149 AA; 17086 MW; 051BB8C47A0114FC CRC64;  
 Query Match 53.8%; Score 85; DB 1; Length 149;  
 Best Local Similarity 53.3%; Pred. No. 1.1e-05;  
 Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLINGINNN 31  
 ||||| : : : : :  
 Db 21 APTSSSKRETQQLQQLQMDLKLLEGVNN 50

## RESULT 14

IL2\_BOVIN STANDARD; PRT; 155 AA.  
 ID IL2\_BOVIN  
 AC P05016;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2 OR IL-2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86205869; PubMed=3517854;  
 RA Carretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D.,  
 RA Gillis S., Cosman D., Baker P.E.;  
 RT "Cloning, sequence, and expression of bovine interleukin 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86205870; PubMed=3486415;  
 RA Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,  
 RA Barr P.J., Magnuson N.S., Magnuson J.A.;  
 RT "Molecular cloning of a functional bovine interleukin 2 cDNA.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).  
 RN [3]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Thymus;  
 RA Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;  
 RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
 CC  
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 CC  
 CC EMBL; M12791; AAA30586.1; -  
 CC EMBL; M13204; AAA21143.1; -  
 CC EMBL; X17201; CAA35062.1; -  
 CC EMBL; X52687; CAA36912.1; -  
 CC HSP; P01585; 3INK  
 CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam; PF00715; IL2; 1.

```
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT CARBOHYD 79 127 BY SIMILARITY.
FT DISULFID 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CONFLICT 66 66 V -> A (IN REF. 2).
SQ SEQUENCE 155 AA; 17627 MW; 816667DFEA052EDF CRC64;

Query Match 45.6%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.001;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKQLQMLNGINN 31
DB 21 APTSSSTGMTKEVKSLLDLQLLEKVRN 50

RESULT 15
IL2_CAPHI
ID IL2_CAPHI STANDARD; PRT; 155 AA.
AC P36835; P79156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rimstad E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beyer J.C.; Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X76063; CAA53664.1; -.
DR EMBL; U34274; AAB38527.1; -.
DR PIR; S38662; S38662.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
```

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:07 ; Search time 24.8889 Seconds  
(without alignments)  
264.918 Million cell updates/sec

Title: US-09-776-781-6  
Perfect score: 158  
Sequence: 1 MAPSSSTKKTQLQLEHLLKLQMLNGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
-13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	93.0	150	4 Q9C001	Q9C001 homo sapien
2	145	91.8	154	6 Q9XS38	Q9XS38 papio hamad
3	135.5	85.8	156	4 Q13169	Q13169 homo sapien
4	134	84.8	139	4 Q16334	Q16334 homo sapien
5	108.5	68.7	155	6 Q9XTB3	Q9XTB3 halichoerus
6	107.5	68.0	66	6 Q9BG74	Q9BG74 canis famil
7	107	67.7	79	6 Q9TV12	Q9TV12 canis famil
8	106	67.1	155	11 Q923T2	Q923T2 sigmodon hi
9	103	65.2	138	11 Q70329	Q70329 mesocricetu
10	99	62.7	133	6 Q9MZ93	Q9MZ93 oryctolagus
11	84	53.2	23	4 Q9UCF5	Q9UCF5 homo sapien
12	78	49.4	154	6 Q9XTB4	Q9XTB4 delphinapte
13	75	47.5	152	11 Q88210	Q88210 cavia porce
14	72	45.6	69	6 Q9GJ84	Q9GJ84 ovis aries
15	72	45.6	155	6 Q9GL83	Q9GL83 capra hircu
16	72	45.6	155	6 Q95KP3	Q95KP3 bubalus bub

17	69	43.7	39	6 Q9BG73	Q9BG73 canis famil
18	69	43.7	150	11 P70291	P70291 mus musculu
19	69	43.7	169	11 Q9QUS8	Q9QUS8 mus musculu
20	67	42.4	150	11 P70294	P70294 mus musculu
21	65.5	41.5	155	11 P70292	P70292 mus musculu
22	62.5	39.6	159	11 P70293	P70293 mus musculu
23	56	35.4	300	2 Q8VW37	Q8VW37 coxiella bu
24	56	35.4	348	12 Q9DHS6	Q9DHS6 yaba-like d
25	53	33.5	251	12 Q9PYU2	Q9PYU2 xestia c-ni
26	53	33.5	452	10 Q9ZV75	Q9ZV75 arabidopsis
27	52	32.9	116	6 Q29138	Q29138 trichechus
28	52	32.9	478	17 Q8TLR6	Q8TLR6 methanosarc
29	51	32.3	517	16 Q8R8R8	Q8R8R8 thermoaer
30	51	32.3	737	16 Q9KTS5	Q9KTS5 vibrio chol
31	51	32.3	866	16 Q25517	Q25517 helicobacte
32	51	32.3	875	16 Q9ZKZ8	Q9ZKZ8 helicobacte
33	50	31.6	95	2 Q9F8U6	Q9F8U6 streptomyce
34	50	31.6	304	16 Q930K5	Q930K5 rhizobium m
35	50	31.6	543	16 Q9KSF8	Q9KSF8 vibrio chol
36	49.5	31.3	104	10 Q9FSQ4	Q9FSQ4 oryza sativ
37	49.5	31.3	367	10 Q9SIF5	Q9SIF5 arabidopsis
38	49.5	31.3	474	10 Q06376	Q06376 brassica na
39	49	31.0	145	16 Q9KAW0	Q9KAW0 bacillus ha
40	48.5	30.7	288	16 Q99TY7	Q99TY7 staphylococ
41	48.5	30.7	366	16 Q98422	Q98422 rhizobium l
42	48	30.4	311	16 Q9CLL6	Q9CLL6 pasteurella
43	48	30.4	398	16 Q50911	Q50911 borrelia bu
44	48	30.4	441	16 Q928V0	Q928V0 listeria in
45	48	30.4	441	16 Q69192	Q69192 listeria mo

#### ALIGNMENTS

#### RESULT 1

ID Q9C001 PRELIMINARY; PRT; 150 AA.  
AC Q9C001;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Interleukin-2 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20545237; PubMed=11093171;  
RA Matesanz F., Delgado C., Fresno M., Alcina A.;  
RT "Allelic selection of human IL-2 gene."  
RL Eur. J. Immunol. 30:3516-3521(2000).  
DR EMBL; AF228636; AAG53575.1; -  
DR HSSP; P01585; 3INK.  
DR InterPro; IPR000779; Interleukin-2.  
DR Pfam; PF00715; IL2; 1.  
DR PRINTS; PD00265; INTERLEUKIN2.  
DR ProDom; PD003649; Interleukin-2; 1.  
DR SMART; SM00189; IL2; 1.  
DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
FT NON\_TER 150 150  
SQ SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;

Query Match 93.0%; Score 147; DB 4; Length 150;  
Best Local Similarity 96.8%; Pred. No. 4.2e-14;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32

Db 21 APTSSSTKKTQLQLEHLLKLQMLNGINNY 51

#### RESULT 2

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Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Aotus lemurinus (Northern gray-necked night monkey),
OS Aotus nancymae (Owl monkey),
OS Aotus nigriceps (black-headed night monkey), and
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -
DR EMBL; U88364; AAD41534.1; -
DR EMBL; U88361; AAD41535.1; -
DR EMBL; U88363; AAD41536.1; -
DR EMBL; U88362; AAD41537.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 91.8%; Score 145; DB 6; Length 154;
Best Local Similarity 93.5%; Pred. No. 8.9e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 21 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 51

RESULT 3
Q13169 PRELIMINARY; PRT; 156 AA.
AC Q13169;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RT "Expression of human IL-2 from gene transfected mouse melanoma cells
RT and its effect on the growth of mouse melanoma.";
RL Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U25676; AAA70092.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.

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DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 85.8%; Score 135.5; DB 4; Length 156;
Best Local Similarity 88.2%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 APTSSS---TKKTKQLQLEHLLKLQMLINGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 21 APTSSSTKTKTKTQLQLEHLLKLQMLINGINNY 54

RESULT 4
Q16334 PRELIMINARY; PRT; 139 AA.
ID Q16334;
AC Q16334;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-95239150; PubMed-7722480;
RA Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD4264.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 139 AA; 15986 MW; 731FBA06D0C63C5 CRC64;

Query Match 84.8%; Score 134; DB 4; Length 139;
Best Local Similarity 90.3%; Pred. No. 3.4e-12;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 17 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 47

RESULT 5
Q9XT83 PRELIMINARY; PRT; 155 AA.
ID Q9XT83;
AC Q9XT83;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 2.
GN Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., Bellevue C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";

```

RL Vet. Immunol. Immunopathol. 67:385-394 (1999).

DR EMBL; AF072871; AAD40848.1; -

DR HSSP; P01585; 3INK.

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN\_2; 1.

SQ SEQUENCE 155 AA; 17860 MW; F18F449AC672241A CRC64;

Query Match 68.7%; Score 108.5; DB 6; Length 155;

Best Local Similarity 71.9%; Pred. No. 2.4e-08;

Matches 23; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

OY 2 AP-TSSSTKKTQLEHLLKLQMLINGNNY 32

|| |||||:|:| || | | | | | | | | | | | | | |

Db 21 APTSSSTKETEQQEQLLDLQLLLNGVNNY 52

RESULT 6

O9BG74

ID O9BG74 PRELIMINARY; PRT; 66 AA.

AC O9BG74; 2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Interleukin 2 (Fragment).

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RA Markus S., Groene A., Baumgaertner W.;

RT "Expression of canine interleukin-2 mRNA in concanavalin A-stimulated

canine lymphocytes."

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF333117; AAK01437.1; -

DR HSSP; P01585; 1IRL.

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

FT NON\_TER 1

FT NON\_TER 66

SQ SEQUENCE 66 AA; 7389 MW; 22A893F79DA2AE47 CRC64;

Query Match 68.0%; Score 107.5; DB 6; Length 66;

Best Local Similarity 68.8%; Pred. No. 1.5e-08;

Matches 22; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

OY 2 AP-TSSSTKKTQLEHLLKLQMLINGNNY 32

|| |||||:|:| || | | | | | | | | | | | | | |

Db 14 APTSSSTKETEQQEQLLDLQLLLNGVNNY 45

RESULT 7

O9TV12

ID O9TV12 PRELIMINARY; PRT; 79 AA.

AC O9TV12;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE Interleukin-2 (Fragment).

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;

RT "Cloning and sequencing of canine IL-2."

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF091131; AAD46989.1; -

DR HSSP; P01585; 1IRL.

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN\_2; 1.

FT NON\_TER 1

FT NON\_TER 79

SQ SEQUENCE 79 AA; 9087 MW; 83079BF8A659BD CRC64;

Query Match 67.7%; Score 107; DB 6; Length 79;

Best Local Similarity 69.0%; Pred. No. 2.1e-08;

Matches 20; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 4 TSSSTKKTQLEHLLKLQMLINGNNY 32

|| |||||:|:| || | | | | | | | | | | | | | |

Db 7 TSSSTKETEQQEQLLDLQLLLNGVNNY 35

RESULT 8

O923T2

ID O923T2 PRELIMINARY; PRT; 155 AA.

AC O923T2;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Interleukin 2.

OS Sigmodon hispidus (Hispid cotton rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Sigmodon.

OX NCBI\_TaxID=42415;

RN [1]

RP SEQUENCE FROM N.A.

RA Darnell M.R., Pletneva L.M., Langley R.J., Blanco J.C., Prince G.A.;

RT "Cloning, expression and purification of cotton rat IL-2."

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF398549; AAK94012.1; -

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR ProDom; PD003649; Interleukin-2; 1.

DR PROSITE; PS00424; INTERLEUKIN\_2; UNKNOWN 1.

SQ SEQUENCE 155 AA; 17627 MW; ACADA865E93291 CRC64;

Query Match 67.1%; Score 106; DB 11; Length 155;

Best Local Similarity 71.0%; Pred. No. 5.8e-08;

Matches 22; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLKLQMLINGNNY 32

|| |||||:|:| || | | | | | | | | | | | | | |

Db 21 APTSSSTKETEQQEQLLDLQLLLNGVNNY 51

RESULT 9

O70329

ID O70329 PRELIMINARY; PRT; 138 AA.

AC O70329;

DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE Interleukin-2 (Fragment).

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

OX NCBI\_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

```

RC TISSUE-SPLEEN;
RX MEDLINE-98234044; PubMed-95731100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046212; AAC40097.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
FT TER 138
SQ SEQUENCE 138 AA; 15739 MW; 3510329958670779 CRC64;

Query Match 65.2%; Score 103; DB 11; Length 138;
Best Local Similarity 71.0%; Pred. No. 1.4e-07;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLKLQMLNGINNY 32
DB 14 APTSSSKKETQQLQLEQLLDQLQELLAGINNY 44

RESULT 10
Q9WZR9
ID Q9WZR9 PRELIMINARY; PRT; 133 AA.
AC Q9WZR9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Interleukin 2 variant ILdelta2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN, AND LYMPH NODE;
RX MEDLINE-20304114; PubMed-10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF169168; AAF86652.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 62.7%; Score 99; DB 6; Length 133;
Best Local Similarity 69.0%; Pred. No. 5.5e-07;
Matches 20; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLKLQMLNGIN 30
DB 21 APTSSSTKETQQLDQLLDQLVLLKGVN 49

RESULT 11
Q9UCF5
ID Q9UCF5 PRELIMINARY; PRT; 23 AA.
AC Q9UCF5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

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DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-93289963; PubMed=8512072;
RA Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 53.2%; Score 84; DB 4; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TSSSTKKTQQLQLEHLLKLQML 24
DB 3 TSXSTKKTQQLQLEHLLKLQML 23

RESULT 12
Q9XT84
ID Q9XT84 PRELIMINARY; PRT; 154 AA.
AC Q9XT84;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99221046; PubMed=10206205;
RA St-Laurent G., Belliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072870; RAD40847.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17652 MW; 42B8D3D41D04F172 CRC64;

Query Match 49.4%; Score 78; DB 6; Length 154;
Best Local Similarity 51.6%; Pred. No. 0.00088;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLKLQMLNGINNY 32
DB 21 APTSSSTENTKQVQSLQDLHLLKEINNH 51

RESULT 13
O88210
ID O88210 PRELIMINARY; PRT; 152 AA.
AC O88210;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SPLEEN;

RA Takeyoshi M., Iwata H., Inoue T.;

RT "Guinea pig Interleukin 2(IL-2) precursor.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB010093; BAA31346.1; -

DR HSSP; P01585; 1IIRL

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

KW Signal.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 152 INTERLEUKIN 2.

SQ SEQUENCE 152 AA; 17271 MW; CAYAC08C1B8DD1FA CRC64;

Query Match 47.5%; Score 75; DB 11; Length 152;

Best Local Similarity 56.7%; Pred. No. 0.0024;

Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLKLQMLNGINN 31

||||| :|| :|| :|| :|| :|| :|| :

DB 21 APTSSSPKQTDRLELLRLDQLTLEGVTS 50

RESULT 14

Q9GJR4

ID Q9GJR4 PRELIMINARY; PRT; 69 AA.

AC Q9GJR4;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Interleukin 2 precursor (Fragment).

GN IL-2.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SHEEP 2, AND SHEEP 1;

RA Luehken G., Prinzenberg E.-M., Hiendleder S., Erhardt G.;

RT "A single strand conformation polymorphism in the ovine interleukin 2

(IL-2) gene.";

RL J. Anim. Sci. 0:0-0(2000).

DR EMBL; AF215687; AAG43986.1; -

DR EMBL; AF213883; AAG35709.1; -

DR HSSP; P01585; 1IIRL

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

KW Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 >69 INTERLEUKIN 2.

FT NON\_TER 69 69

SQ SEQUENCE 69 AA; 7711 MW; B8768C23BB34D1AE CRC64;

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Best Local Similarity 45.6%; Score 72; DB 6; Length 69;

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLKLQMLNGINN 31

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DB 21 APTSSSTGNTMKVKSLLDLQLLLEKVN 50

RESULT 15

Q9GL83

ID Q9GL83 PRELIMINARY; PRT; 155 AA.

AC Q9GL83;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Interleukin 2.

GN IL-2.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Caprinae; Capra.

OX NCBI\_TaxID=9925;

RN [1]

RP SEQUENCE FROM N.A.

RA Ying Q.H., Li X.R., Pan J.Y.;

RT "Cloning of the goat IL-2 gene and its expression in E.coli.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307018; AAG28783.1; -

DR HSSP; P01585; 3INK

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN\_2; 1.

SQ SEQUENCE 155 AA; 17605 MW; EEEB2DE18F5469AA CRC64;

Query Match

Best Local Similarity 45.6%; Score 72; DB 6; Length 155;

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLKLQMLNGINN 31

||||| :|| :|| :|| :|| :|| :|| :

DB 21 APTSSSTGNTMKVKSLLDLQLLLEKVN 50

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GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2003, 10:05:07 ; Search time 8.12698 Seconds  
(without alignments)  
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Title: US-09-776-781-6  
 Perfect score: 158  
 Sequence: 1 MAPSSSTKKTQLOIEHLLKLOWTINGINNY 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	149	94.3	381	10	US-09-822-698A-5		Sequence 5, Appli
2	147	93.0	133	9	US-10-051-657A-1		Sequence 1, Appli
3	147	93.0	133	10	US-09-766-543-8		Sequence 8, Appli
4	147	93.0	153	10	US-09-149-721-3		Sequence 3, Appli
5	147	93.0	153	10	US-09-923-246-111		Sequence 11, App
6	143	90.5	133	10	US-09-766-543-14		Sequence 14, Appl
7	143	90.5	331	10	US-09-033-525-2		Sequence 2, Appli
8	57	36.1	43	10	US-09-835-147-11		Sequence 11, Appl
9	57	36.1	454	10	US-09-835-147-6		Sequence 6, Appli
10	57	36.1	478	10	US-09-835-147-8		Sequence 8, Appli
11	57	36.1	487	10	US-09-835-147-26		Sequence 26, Appl
12	51	32.3	751	10	US-09-881-752A-280		Sequence 280, App
13	51	32.3	866	10	US-09-815-242-11373		Sequence 11373, A
14	50	31.6	37	9	US-10-142-120-1		Sequence 1, Appli
15	47	29.7	226	10	US-09-796-149-5		Sequence 5, Appli
16	47	29.7	256	9	US-10-013-379-25		Sequence 25, Appl
17	47	29.7	515	10	US-09-925-300-1285		Sequence 1285, Ap
18	46	29.1	1403	9	US-10-108-605-93		Sequence 93, Appl
19	44	27.8	284	10	US-09-810-997-1		Sequence 1, Appli

## ALIGNMENTS

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RESULT 1
US-09-822-698A-5
; SEQUENCE 5, Application US/09822698A-5
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoozenboom, Hendricus R.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUC1N-1 Specific
; FILE REFERENCE: DYX-015-1 US
; CURRENT APPLICATION NUMBER: US/09/8-538
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific i
US-09-822-698A-5

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Query Match 94.3%; Score 149; DB 10; Length 381;  
Best Local Similarity 93.8%; Pred. NO. 6.2e-15;  
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLKLQMLNGINNY 32  
:  
Db 248 LAPSSSTKKTQLEHLLDLOMLNGINNY 279

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RESULT 2
US-10-051-657A-1
; Sequence 1, Application US/10051657A
; Patent No. US20020164300A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelly, Ruth
; TITLE OF INVENTION: Interleukin-2 M
; FILE REFERENCE: MSB-7257
; CURRENT APPLICATION NUMBER: US/10/0

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; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 133
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-051-657A-1

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Query Match 93.0%; Score 147; DB 9; Length 133;  
Best Local Similarity 96.8%; Pred. NO. 3.5e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels

Qy	2	A	P	T	S	S	T	K	K	T	Q	L	E	H	L	L	K	I	Q	M	I	L	N	G	I	N	Y	32
Db	1	A	P	T	S	S	T	K	K	T	Q	L	E	H	L	L	D	L	Q	M	I	L	N	G	I	N	Y	31

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RESULT 3
US-09-766-543-8
; Sequence 8, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09766.543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial S
US-09-766-543-8

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Query Match 93.0%; Score 147; DB 10; Length 133;  
Best Local Similarity 96.8%; Pred. NO. 3.5e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32  
 |||||  
 Db 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31  
 |||||

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RESULT 4
US-09-149-721-3
; Sequence 3, Application US/09149721
; Patent No. US20020058795A1
; GENERAL INFORMATION:
; APPLICANT: Mummer, Russ; Tagliaferri, Frank
; TITLE OF INVENTION: HYDROPHOBIC GLYCOSYLAMINE DERIVATIVES, COMPOSITIONS, AND METHODS
; FILE REFERENCE: 237/023
; CURRENT APPLICATION NUMBER: US/09/149,721
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 60/058,259
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo Saplens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of human IL-2
US-09-149-721-3

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Best Local Similarity	96.8%;	Pred. NO. 4.1e-15;		
Matches 30;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

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<b>D<sub>b</sub></b>	<b>21</b>	A P T S S T K K T Q L Q E H L L L D L Q M I L G I N N Y	<b>51</b>

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RESULT 5
US-09-923-246-111
; Sequence 111, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Ronald D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-111

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Query Match	Score	DB	Length
Best Local Similarity	93.0%	147	153
Matches	96.8%	Pred. No. 4.1e-15;	
30; Conservative	0;	Mismatches 1;	
		Indels	0;
		Gaps	0;

		Qy	2	A P T S S T K K T Q L Q E H L L K I Q M I N G I N Y	32
		Dd	21	A P T S S T K K T Q L Q E H L L D L Q M I N G I N Y	51

```

RESULT 6
US-09-766-543-14
; Sequence 14, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09766.543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence

```





; PRIOR FILING DATE: 1999-10-13  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 478  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
 ; OTHER INFORMATION: construct of human CD39  
 ; US-09-835-147-8

Query Match 36.1%; Score 57; DB 10; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 0.65;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13  
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 Db 25 APTSSSTKKTQL 36

RESULT 11  
 US-09-835-147-26  
 ; Sequence 26, Application US/09835147  
 ; Patent No. US2002002277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maliszewski, Charles R.  
 ; APPLICANT: Gayle III, Richard B.  
 ; APPLICANT: Price, Virginia L.  
 ; APPLICANT: Gimpel, Steven D.  
 ; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
 ; FILE REFERENCE: 2879-US  
 ; CURRENT APPLICATION NUMBER: US/09/835,147  
 ; CURRENT FILING DATE: 2001-04-13  
 ; PRIOR FILING DATE: 1998-10-16  
 ; PRIOR APPLICATION NUMBER: US 60/104,585  
 ; PRIOR FILING DATE: 1998-10-16  
 ; PRIOR APPLICATION NUMBER: US 60/107,466  
 ; PRIOR FILING DATE: 1998-11-06  
 ; PRIOR APPLICATION NUMBER: US 60/149,010  
 ; PRIOR FILING DATE: 1999-08-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/22955  
 ; PRIOR FILING DATE: 1999-10-13  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 26  
 ; LENGTH: 487  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
 ; OTHER INFORMATION: construct of human CD39  
 ; US-09-835-147-26

Query Match 36.1%; Score 57; DB 10; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 0.66;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13  
 |||||  
 Db 25 APTSSSTKKTQL 36

RESULT 12  
 US-09-881-752A-280  
 ; Sequence 280, Application US/09881752A  
 ; Patent No. US20020115078A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kleanthous, Harold  
 ; APPLICANT: Al-Garawi, Amal  
 ; APPLICANT: Miller, Charles  
 ; APPLICANT: Tomb, Jean-Francois  
 ; APPLICANT: Coenen, Raymond P.  
 ; TITLE OF INVENTION: Identification of Polynucleotides

; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in t  
 ; TITLE OF INVENTION: Genome  
 ; FILE REFERENCE: 06132/041002  
 ; CURRENT APPLICATION NUMBER: US/09/881,752A  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: US 08/833,457  
 ; PRIOR FILING DATE: 1997-04-01  
 ; NUMBER OF SEQ ID NOS: 370  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 280  
 ; LENGTH: 751  
 ; TYPE: PRT  
 ; ORGANISM: Helicobacter pylori  
 ; US-09-881-752A-280

Query Match 32.3%; Score 51; DB 10; Length 751;  
 Best Local Similarity 42.9%; Pred. No. 9;  
 Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLEHLLKLQMLNGINNY 32  
 |||||  
 Db 509 SESQKKDFIKLFGKILKLENILNSFENF 536

RESULT 13  
 US-09-815-242-11373  
 ; Sequence 11373, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Genes in  
 ; TITLE OF INVENTION: Prokaryotes  
 ; FILE REFERENCE: ELITRA.011A  
 ; CURRENT APPLICATION NUMBER: US/09/815,242  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 14110  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11373  
 ; LENGTH: 866  
 ; TYPE: PRT  
 ; ORGANISM: Helicobacter pylori  
 ; US-09-815-242-11373

Query Match 32.3%; Score 51; DB 10; Length 866;  
 Best Local Similarity 42.9%; Pred. No. 11;  
 Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLEHLLKLQMLNGINNY 32  
 |||||  
 Db 624 SESQKKDFIKLFGKILKLENILNSFENF 651

RESULT 14  
US-10-142-120-1  
; Sequence 1, Application US/10142120  
; Patent No. US20020164302A1  
; GENERAL INFORMATION:  
; APPLICANT: Epstein, Alan L.  
; TITLE OF INVENTION: VASOPRESSIN-RECEPTOR ENHANCING PEPTIDE FRAGMENT OF HUMAN INTERLEUKIN-  
; FILE REFERENCE: 1920-325D2-09801297  
; CURRENT APPLICATION NUMBER: US/10/142,120  
; CURRENT FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 09/443,061  
; PRIOR FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: 08/806,121  
; PRIOR FILING DATE: 1996-12-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-142-120-1

Query Match 31.6%; Score 50; DB 9; Length 37;  
Best Local Similarity 90.08; Pred. No. 0.33;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 QMILNGINNY 32  
:|||||  
Db 1 EMILNGINNY 10

RESULT 15  
US-09-796-149-5  
; Sequence 5, Application US/09796149  
; Patent No. US20020035079A1  
; GENERAL INFORMATION:  
; APPLICANT: Univ. of Southern California  
; TITLE OF INVENTION: Mutated cyclin G1 protein  
; FILE REFERENCE: 4-31342A/USC  
; CURRENT APPLICATION NUMBER: US/09/796,149  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-149-5

Query Match 29.7%; Score 47; DB 10; Length 226;  
Best Local Similarity 60.08; Pred. No. 8.4;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TKKTQLQLEHLLKL 22  
||| |::|||:  
Db 82 TKKQVLRMEHLVLKV 96

Search completed: February 20, 2003, 10:08:32  
Job time : 8.12698 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:00:37 ; Search time 30.0159 Seconds  
(without alignments)  
137.619 Million cell updates/sec

Title: US-09-776-781-8

Perfect score: 153

Sequence: 1 APTSSSTKTKQLQLEHLLKQLMILGINNY 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID22/qcgdata/geneseq/geneseq-embl/AA1981.DAT.\*
- 3: /SID22/qcgdata/geneseq/geneseq-embl/AA1982.DAT.\*
- 4: /SID22/qcgdata/geneseq/geneseq-embl/AA1983.DAT.\*
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- 6: /SID22/qcgdata/geneseq/geneseq-embl/AA1985.DAT.\*
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- 11: /SID22/qcgdata/geneseq/geneseq-embl/AA1990.DAT.\*
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- 13: /SID22/qcgdata/geneseq/geneseq-embl/AA1992.DAT.\*
- 14: /SID22/qcgdata/geneseq/geneseq-embl/AA1993.DAT.\*
- 15: /SID22/qcgdata/geneseq/geneseq-embl/AA1994.DAT.\*
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- 19: /SID22/qcgdata/geneseq/geneseq-embl/AA1998.DAT.\*
- 20: /SID22/qcgdata/geneseq/geneseq-embl/AA1999.DAT.\*
- 21: /SID22/qcgdata/geneseq/geneseq-embl/AA2000.DAT.\*
- 22: /SID22/qcgdata/geneseq/geneseq-embl/AA2001.DAT.\*
- 23: /SID22/qcgdata/geneseq/geneseq-embl/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	153	100.0	31	23 ABB79535	Interleukin-2 pept
2	153	100.0	32	23 ABB79534	Interleukin-2 pept
3	153	100.0	133	21 AAY53825	Amino acid sequenc
4	150	98.0	133	21 AAY53829	Amino acid sequenc
5	149	97.4	133	21 AAY53828	Amino acid sequenc
6	149	97.4	134	8 AAP70573	Sequence of segmen
7	148	96.7	133	21 AAY53830	Amino acid sequenc
8	148	96.7	133	21 AAY53901	Amino acid sequenc
9	147	96.1	58	12 AAR11015	Human interleukin-
10	147	96.1	60	11 AAR06836	Human IL-2 N-termi

11	147	96.1	60	15 AAR48245	Human Interleukin-
12	147	96.1	88	17 AAR95433	Interleukin-2 ALPH
13	147	96.1	96	15 AAR68899	Human pro-insulin
14	147	96.1	96	16 AAR78662	Fusion protein con
15	147	96.1	120	6 AAP50864	Sequence of interl
16	147	96.1	128	12 AAR10906	Interleukin-2 muta
17	147	96.1	129	12 AAR10905	Interleukin-2 muta
18	147	96.1	129	12 AAR10908	Interleukin-2 muta
19	147	96.1	130	12 AAR10907	Interleukin-2 muta
20	147	96.1	131	4 AAP30044	Sequence of interl
21	147	96.1	131	6 AAP50217	Sequence of human
22	147	96.1	132	12 AAR10901	Interleukin-2 muta
23	147	96.1	132	12 AAR10902	Interleukin-2 muta
24	147	96.1	132	12 AAR10903	Interleukin-2 muta
25	147	96.1	132	12 AAR10904	Interleukin-2 muta
26	147	96.1	132	23 ABB79536	Human interleukin-
27	147	96.1	133	5 AAP40048	Sequence of an int
28	147	96.1	133	5 AAP40044	Sequence of mature
29	147	96.1	133	6 AAP50163	Sequence of the hu
30	147	96.1	133	6 AAP50857	Sequence of interl
31	147	96.1	133	6 AAP50858	Sequence of interl
32	147	96.1	133	6 AAP50859	Sequence of interl
33	147	96.1	133	6 AAP50860	Sequence of interl
34	147	96.1	133	6 AAP50861	Sequence of interl
35	147	96.1	133	6 AAP50862	Sequence of interl
36	147	96.1	133	6 AAP50863	Sequence of interl
37	147	96.1	133	7 AAP60833	Oxidation resistan
38	147	96.1	133	7 AAP60834	Oxidation resistan
39	147	96.1	133	7 AAP60835	Oxidation resistan
40	147	96.1	133	7 AAP60836	Oxidation resistan
41	147	96.1	133	7 AAP60837	Oxidation resistan
42	147	96.1	133	7 AAP60838	Oxidation resistan
43	147	96.1	133	7 AAP61100	Sequence of interl
44	147	96.1	133	7 AAP61651	Antigenic fragment
45	147	96.1	133	7 AAP61725	Plasmid pILOx135-8

ALIGNMENTS

RESULT 1

ABB79535

ID ABB79535 standard; Peptide; 31 AA.

XX

AC ABB79535;

XX

DT 23-SEP-2002 (first entry)

XX

DE Interleukin-2 peptide IP131 (D20K).

XX

KW IP131; interleukin-2; human; gene; gene therapy; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 20

FT /note= "wild-type Asp substituted by Lys"

XX

PN US2002044935-A1.

XX

PD 18-APR-2002.

XX

PF 06-FEB-2001; 2001US-0776781.

 XX |  || PR | 16-JUL-1998; 98US-0116594. |
PR	12-SEP-2000; 2000US-0660465.
XX	
PA	(INSP ) INST PASTEUR.
XX	
PI	Thereze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;
PI	Mazie J;
XX	

DR WPI: 2002-546505/58.  
 DR N-PSDB; ABN84296.

PT New peptides derived from Interleukin 2 designated Ip130 and Ip131 are  
 PT useful as therapeutic agents in the treatment of patients deficient in  
 PT IL-2 activity -

XX Claim 18; Page -: 53pp; English.

XX The present sequence is the protein sequence for Ip131 D20K. The  
 CC sequence is based on the human interleukin-2 (IL-2) peptide Ip130  
 CC (see ABN84292) by the addition of a C-terminal Tyr residue, and  
 CC substitution of the native Asp-20 residue by Lys. Asp-20 is  
 CC located in a region of IL-2 that directly influences interaction of  
 CC the cytokine with its receptor (IL-2R). An antibody that binds to  
 CC the peptide is claimed, and is preferably an antibody produced by  
 CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting  
 CC the presence or activity of involves contacting a sample with  
 CC Ip131 D20K, and detecting whether binding occurs. A claimed method  
 CC for inhibiting IL-2R activity involves contacting IL-2R with the  
 CC peptide. A claimed method for inducing IL-2 activity in a patient  
 CC comprises administering Ip131 D20K to the patient. A vector  
 CC containing DNA encoding the peptide is claimed, and is used in a  
 CC claimed method for treating a patient deficient in IL-2 activity.  
 CC Also claimed are peptides corresponding to Ip131 D20K but  
 CC containing conservative amino acid substitutions, i.e. change of  
 CC non-polar R-groups but other non-polar R-groups, change of  
 CC uncharged polar R-groups by other uncharged polar R-groups,  
 CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by  
 CC Gln, and vice versa. The peptide induces SHC phosphorylation or  
 CC induction of the SHC/MAPK pathway. Antibodies specific for the  
 CC peptide are useful for treatment or prevention of undesirable  
 CC immune reactions such as graft rejection, or autoimmune disorders  
 CC such as rheumatoid arthritis.  
 CC Note: The present sequence is not shown in the specification but  
 CC is derived from the IL131 sequence given in page 2 (see ABB79534)  
 CC by removal of the N-terminal Met residue.

XX SQ Sequence 31 AA;

Query Match 100.0%; Score 153; DB 23; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
 |||||  
 Db 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31

RESULT 2  
 ABB79534  
 ID ABB79534 standard; Peptide; 32 AA.

XX ABB79534;

XX 23-SEP-2002 (first entry)

DE Interleukin-2 peptide Ip131 (D20K).

XX Ip131; Interleukin-2; human; gene; gene therapy; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 21 /note= "wild-type Asp substituted by Lys"

XX US2002044935-A1.

XX 18-APR-2002.

XX 06-FEB-2001; 2001US-0776781.

XX

PR 16-JUL-1998; 98US-0116594.  
 PR 12-SEP-2000; 2000US-0660465.

PA (INSP ) INST PASTEUR.

XX Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;  
 PI Mazie J;

XX WPI: 2002-546505/58.  
 DR N-PSDB; ABN84295.

XX New peptides derived from Interleukin 2 designated Ip130 and Ip131 are  
 PT useful as therapeutic agents in the treatment of patients deficient in  
 PT IL-2 activity -

XX Claim 18; Page 2; 53pp; English.

XX The present sequence is the protein sequence for Ip131 D20K. The  
 CC sequence is based on the human interleukin-2 (IL-2) peptide Ip130  
 CC (see ABN84292) by the addition of a C-terminal Tyr residue, and  
 CC substitution of the native Asp-20 residue by Lys. Asp-20 is  
 CC located in a region of IL-2 that directly influences interaction of  
 CC the cytokine with its receptor (IL-2R). An antibody that binds to  
 CC the peptide is claimed, and is preferably an antibody produced by  
 CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting  
 CC the presence or activity of involves contacting a sample with  
 CC Ip131 D20K, and detecting whether binding occurs. A claimed method  
 CC for inhibiting IL-2R activity involves contacting IL-2R with the  
 CC peptide. A claimed method for inducing IL-2 activity in a patient  
 CC comprises administering Ip131 D20K to the patient. A vector  
 CC containing DNA encoding the peptide is claimed, and is used in a  
 CC claimed method for treating a patient deficient in IL-2 activity.  
 CC Also claimed are peptides corresponding to Ip131 D20K but  
 CC containing conservative amino acid substitutions, i.e. change of  
 CC non-polar R-groups but other non-polar R-groups, change of  
 CC uncharged polar R-groups by other uncharged polar R-groups,  
 CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by  
 CC Gln, and vice versa. The peptide induces SHC phosphorylation or  
 CC induction of the SHC/MAPK pathway. Antibodies specific for the  
 CC peptide are useful for treatment or prevention of undesirable  
 CC immune reactions such as graft rejection, or autoimmune disorders  
 CC such as rheumatoid arthritis.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 153; DB 23; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
 |||||  
 Db 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32

RESULT 3

AAV53825

ID AAV53825 standard; Protein; 133 AA.

XX AAV53825;

XX 13-MAR-2000 (first entry)

XX Amino acid sequence of human interleukin-2 (IL-2) mutein D20K.

XX Human; Interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;  
 KW malignant melanoma; autoimmune disease; infectious disease;  
 KW immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;  
 KW gene therapy.

XX Synthetic.

OS Homo sapiens.

XX

```

EH Key Location/Qualifiers
FT Misc-difference 20 /note= "wild type Asp has been replaced with Lys"
XX
XX
XX
XX WO9960128-A1.
XX
XX 25-NOV-1999.
XX
XX 13-MAY-1999; 99WO-US10643.
XX
XX 15-MAY-1998; 98US-0080080.
XX
XX (FARB ) BAYER CORP.
XX
XX Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX
XX WPI; 2000-086598/07.
XX
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer -
XX
XX Example 5; Page -: 80pp; English.
XX
XX AAY53822-66 represent human interleukin-2 (IL-2) muteins, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
XX
SQ Sequence 133 AA;
Query Match 100.0%; Score 153; DB 21; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
| | | | | | | | | | | | | | | | | | | | |
DB 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
| | | | | | | | | | | | | | | | | | | | |
RESULT 4
AAY53829
ID AAY53829 standard; Protein; 133 AA.
XX
XX AAY53829;
XX
XX 13-MAR-2000 (first entry)
XX
XX Amino acid sequence of human interleukin-2 (IL-2) mutein D20R.
XX
XX Human; interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;
XX malignant melanoma; autoimmune disease; infectious disease;
XX immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;
XX gene therapy.
XX
XX Synthetic.
OS

```

```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 20 /note= "wild type Asp has been replaced with Arg"
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XX
XX WO9960128-A1.
XX
XX 25-NOV-1999.
XX
XX 13-MAY-1999; 99WO-US10643.
XX
XX 15-MAY-1998; 98US-0080080.
XX
XX (FARB ) BAYER CORP.
XX
XX Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX
XX WPI; 2000-086598/07.
XX
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer -
XX
XX Example 5; Page -: 80pp; English.
XX
XX AAY53822-66 represent human interleukin-2 (IL-2) muteins, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
XX
SQ Sequence 133 AA;
Query Match 98.0%; Score 150; DB 21; Length 133;
Best Local Similarity 96.8%; Pred. No. 1.5e-13;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
| | | | | | | | | | | | | | | | | | | | |
DB 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
| | | | | | | | | | | | | | | | | | | | |
RESULT 5
AAY53828
ID AAY53828 standard; Protein; 133 AA.
XX
XX AAY53828;
XX
XX 13-MAR-2000 (first entry)
XX
XX Amino acid sequence of human interleukin-2 (IL-2) mutein D20Q.
XX
XX Human; interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;
XX malignant melanoma; autoimmune disease; infectious disease;
XX immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;
XX gene therapy.
XX
XX

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PI Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX WPI; 2000-086598/07.
XX
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer -
XX
XX Example 5; Page -: 80pp; English.
XX
XX AAY53822-66 represent human interleukin-2 (IL-2) muteins, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
XX
XX Sequence 133 AA;
XX
XX Query Match 96.7%; Score 148; DB 21; Length 133;
XX Best Local Similarity 96.8%; Pred. No. 3e-13;
XX Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX DB 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX
XX RESULT 8
XX AAY53901
XX ID AAY53901 standard; Protein; 133 AA.
XX AC AAY53901;
XX DT 13-MAR-2000 (first entry)
XX
XX DE Amino acid sequence of human interleukin-2 (IL-2) mutein D20N.
XX
XX KW Human; interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;
XX malignant melanoma; autoimmune disease; infectious disease;
XX immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;
XX gene therapy.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 20
XX FT /note= "wild type Asp has been replaced with Asn"
XX
XX PN W09560128-A1.
XX PD
XX PD 25-NOV-1999.
XX
XX PF 13-MAY-1999; 99WO-US10643.
XX
XX PR 15-MAY-1998; 98US-0080080.
XX
XX

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PA (FARB ) BAYER CORP.
XX
XX Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX WPI; 2000-086598/07.
XX
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer -
XX
XX Example 5; Page -: 80pp; English.
XX
XX The present sequence is a human interleukin-2 (IL-2) mutein, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
XX
XX Sequence 133 AA;
XX
XX Query Match 96.7%; Score 148; DB 21; Length 133;
XX Best Local Similarity 96.8%; Pred. No. 3e-13;
XX Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX DB 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX
XX RESULT 9
XX AAR11015
XX ID AAR11015 standard; Peptide; 58 AA.
XX AC AAR11015;
XX DT 13-MAY-1991 (first entry)
XX
XX DE Human interleukin-2-derived stabiliser peptide.
XX
XX KW interleukin-2; IL-2; gag 24; gp 41; gp 36; HIV detection.
XX
XX OS Homo sapiens.
XX
XX PN EP416673-A.
XX
XX PD 13-MAR-1991.
XX
XX PF 02-AUG-1990; 90EP-0202108.
XX
XX PR 03-AUG-1989; 89CU-0000149.
XX
XX (INGE-) CENT ING GENETICA.
XX
XX Novoa Perez LI, Machado Lahera JA, Fernandez Maso JR;
XX Benitez Fuentes JV, Narciandi Diaz RE, Rodriguez Reinoso JL;
XX Estrada Garcia MP, Garcia Suarez J, Herrera Martinez LS;
XX

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DR WPI; 1991-075192/11.
XX N-PSDB; AAQ10898.
PT Method for expressing heterologous proteins - as fusion protein,
XX using vector contg. stabilising sequence
XX
XX Claim 2; Page 10; 18pp; English.
XX
CC The sequence corresponds to the first 58 amino acid residues of
CC human IL-2. It forms part of a fusion protein, linked to a
CC heterologous protein. The heterologous protein is preferably gag 24
CC or a fragment of gp 41 of HIV-1 or it is a fragment of gp 36 of
CC HIV-2. Such fusion proteins can be used to detect antibodies to
CC these proteins. See also AAQ10899-Q10903.
XX
SQ Sequence 58 AA;

Query Match 96.1%; Score 147; DB 12; Length 58;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32

RESULT 10
AAR06838
ID AAR06838 standard; protein; 60 AA.
XX
AC AAR06838;
XX
XX 14-JAN-1991 (first entry)
XX
DE Human IL-2 N-terminal transcript of plasmid pTl3S.
XX
KW Bovine tuberculosis; Interleukin-2; IL-2; plasmid pTl3S.
XX
OS Mycobacterium bovis.
XX
XX JP02195895-A.
XX
XX 02-AUG-1990.
XX
XX 24-JAN-1989; 89JP-0013270.
XX
XX 24-JAN-1989; 89JP-0013270.
XX
XX (AJIN ) AJINOMOTO KK.
XX
DR WPI; 1990-278851/37.
DR N-PSDB; AAQ05976.
XX
XX BCG bacteria derived immuno:protein MPB70 - can be used as
XX diagnostic agent used to determine bovine tuberculosis.
XX
XX Disclosure; Fig 2; 11pp; Japanese.
XX
CC Immunoprotein MPB 70 encoding sequence may be incorporated into
CC plasmid pTl3S with an N-terminal fragment of human IL-2. The plasmid
CC may be used to transform an expression system giving a fusion
CC protein which may be used as a diagnostic agent for bovine
CC tuberculosis infection.
XX
SQ Sequence 60 AA;

Query Match 96.1%; Score 147; DB 11; Length 60;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32

Query Match 96.1%; Score 147; DB 15; Length 60;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32

RESULT 12
AAR95433
ID AAR95433 standard; Protein; 88 AA.
XX
XX AAR95433;
XX
XX 17-SEP-1996 (first entry)
XX
DE Interleukin-2 ALPHA segment.
XX
KW Multifunctional protein; targetted hetero-association;
```

```
RESULT 11
AAR48245
ID AAR48245 standard; Protein; 60 AA.
XX
XX AAR48245;
XX
XX 12-JUL-1994 (first entry)
XX
DE Human Interleukin-2.
XX
KW non-coding region; coding region; resonance; interaction; IL-2;
KW optimisation; degenerate sequence; plasmid pTl3SMco; pT9-11;
KW gene expression; regulation; recombinant protein production;
KW Interleukin-2; interleukin-6.
XX
OS Homo sapiens.
XX
XX FR2692594-A.
XX
XX 24-DEC-1993.
XX
XX 22-JUN-1992; 92FR-0007571.
XX
XX 22-JUN-1992; 92FR-0007571.
XX
XX (PERE/) PEREZ J.
XX
XX Perez J;
XX
XX WPI; 1994-028256/04.
XX
XX N-PSDB; AAQ55629, AAQ55630.
XX
XX Application of optimised gene expression - for scientific,
XX Industrial and therapeutic purposes
XX
XX Disclosure; Fig 28 and Fig 29; 110pp; French.
XX
XX Resonances between coding and non-coding regions were measured for
XX the native human IL-2 gene in plasmid pT911 (see AAQ55630) and a
XX synthetic IL-2 gene (AAQ55629) in which alternative, degenerate
XX codons were used in order to introduce additional restriction
XX sites. It was found that the degenerate changes greatly upset the
XX "natural order" between coding and non-coding regions; as a result,
XX the amount of protein expressed by the degenerate gene is likely to
XX be adversely affected. The inventors have proposed an "optimised"
XX IL-2 gene with the aim of increasing the amount of protein expressed
XX by the gene. (N.B. the sequence is also described as
XX Interleukin-6).
XX
SQ Sequence 60 AA;

Query Match 96.1%; Score 147; DB 15; Length 60;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32
```

KW protein assembly; antibody engineering; interleukin-2; IL-2;  
 KW cytokine; tumour; therapy.  
 XX Synthetic.  
 XX WO9613583-A2.  
 PN 09-MAY-1996.  
 PD 20-OCT-1995; 95WO-EP04117.  
 PF 20-OCT-1994; 94EP-0116558.  
 PR (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.  
 XX Lupas A, Pack P;  
 XX WPI; 1996-239496/24.  
 DR N-PSDB; AAT15267.  
 XX Targetted hetero-association of recombinant proteins to  
 PT multi-functional complexes - useful for therapeutic and diagnostic  
 PT purposes  
 XX Example 3; Fig 13; 34pp; English.  
 PS Human interleukin-2 (IL-2) can be used as an assembly device for  
 XX the targeted hetero-association of recombinant proteins. The IL-2  
 CC is segmented between His79 and Lys80 to form ALPHA (AAR95433) and  
 CC BETA (AAR95434) segments encoded by MroI-Asci-HindIII gene cassettes  
 CC (AAT15267 and AAT15268, respectively). The device combines the low  
 CC immunogenicity of the plasmatic protein with a preferable effector  
 CC function of the native-like cytokine structure and an inter-  
 CC segmental cysteine bridge (Cys58-Cys105) after assembly. The  
 CC combination of 1 or more antibody fragments against tumour antigens  
 CC with additional cytokines, e.g. IL-6 or IL-12, targets the  
 CC multi-cytokine complex directly to the tumour.  
 XX  
 SQ Sequence 88 AA;  
 Query Match 96.1%; Score 147; DB 17; Length 88;  
 Best Local Similarity 96.8%; Pred. No. 2.6e-13;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31  
 Db 3 APTSSSTKKTQLQLEHLLKQLMILNGINNY 33  
 RESULT 13  
 AAR68899  
 ID AAR68899 standard; peptide; 96 AA.  
 XX AAR68899;  
 AC AAR68899;  
 XX 02-MAR-1995 (first entry)  
 DT Human pro-insulin 2.  
 XX Pro-insulin; A-chain; B-chain; C-chain; disulphide;  
 KW mercaptan; chaotropic agent.  
 XX Homo sapiens.  
 OS EP600372-A.  
 XX 08-JUN-1994.  
 PD 25-NOV-1993; 93EP-0118993.  
 XX 02-DEC-1992; 92DE-4240420.  
 PR (FARH ) HOECHST AG.  
 PA

XX Gerl M, Ludwig J, Obermeier R, Sabel W;  
 PI WPI; 1994-177718/22.  
 XX Prodn. of pro-insulin with correct di: sulphide bridges - by  
 PT treating recombinant precursor protein with mercaptan in alkali  
 PT and in presence of chaotropic agent, then isolation on  
 PT hydrophobic resin  
 XX Disclosure; Page 11; 15pp; German.  
 PS Pro-insulin is produced by treating recombinant precursor protein  
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in  
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,  
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.  
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and  
 CC desorbing the pro-insulin. This method produces pro-insulin with  
 CC correctly bonded Cys bridges. Compared with known methods it  
 CC involves fewer stages (esp. no sulphitolyis or cyanogen bromide  
 CC cleavage) and overall losses during purification are reduced, i.e.  
 CC the process is quicker and gives better yields.  
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.  
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.  
 XX  
 SQ Sequence 96 AA;  
 Query Match 96.1%; Score 147; DB 15; Length 96;  
 Best Local Similarity 96.8%; Pred. No. 2.9e-13;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31  
 Db 2 APTSSSTKKTQLQLEHLLKQLMILNGINNY 32  
 RESULT 14  
 AAR78662  
 ID AAR78662 standard; protein; 96 AA.  
 XX AAR78662;  
 AC AAR78662;  
 XX 03-APR-1996 (first entry)  
 DT Fusion protein contg. proinsulin sequence 3.  
 XX Proinsulin; post-translational modification; recombinant production;  
 KW protein folding; conformation.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 XX Region 41..44  
 FT /label= R2  
 FT /note= "a peptide of 4 amino acids"  
 FT Peptide 45..74  
 FT /label= R1-(B2-B29)-Y  
 FT /note= "human insulin B-chain"  
 FT Region 75  
 FT /label= X  
 FT Peptide 76..96  
 FT /label= Gly-(A2-A20)-R3  
 FT /note= "human insulin A-chain"  
 XX EP668292-A2.  
 PN 23-AUG-1995.  
 XX 09-FEB-1995; 95EP-0101748.  
 PF 18-FEB-1994; 94DE-4405179.  
 PR (FARH ) HOECHST AG.  
 PA



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:27 ; Search time 28.0476 Seconds  
(without alignments)  
106.254 Million cell updates/sec

Title: US-09-776-781-8  
Perfect score: 153  
Sequence: 1 APTSSSTKTKQLQLHLLKLMILNINNY 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.73:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.1	153	1	ICHU2
2	147	96.1	153	1	ICHU2
3	107	69.9	154	2	JN0698
4	97	63.4	155	2	A31278
5	96	62.7	154	2	S16241
6	95	62.1	155	2	S33509
7	85	55.6	149	2	S31391
8	72	47.1	155	2	S38662
9	72	47.1	155	2	S11488
10	72	47.1	155	2	I45913
11	69	45.1	169	2	S37289
12	64	41.8	169	1	ICMS2
13	61	39.9	189	2	H64307
14	54	35.3	1061	1	HGLJG4
15	53	34.6	357	2	S12169
16	53	34.6	452	2	B84483
17	52.5	34.3	60	2	I68870
18	51.5	33.7	62	2	I54512
19	51.5	33.7	415	2	I51637
20	51	33.3	737	2	G82262
21	51	33.3	866	2	F64625
22	51	33.3	875	2	B17890
23	50.5	33.0	72	2	I68871
24	50.5	33.0	741	2	A45771
25	50	32.7	304	2	F95285
26	50	32.7	543	2	F62217
27	49.5	32.4	367	2	E84453
28	49.5	32.4	474	2	S31712
29	49	32.0	145	2	H83921

30	48.5	31.7	452	2	G54679
31	48	31.4	398	2	B70209
32	48	31.4	441	2	AB1367
33	48	31.4	441	2	AC1736
34	48	31.4	765	2	S76795
35	48	31.4	1964	2	A59282
36	47.5	31.0	127	1	NR80K2
37	47.5	31.0	244	2	T11685
38	47.5	31.0	288	2	B99930
39	47	30.7	257	2	S39521
40	47	30.7	307	2	T46103
41	47	30.7	406	2	S24788
42	47	30.7	432	2	S08277
43	47	30.7	511	2	D71687
44	47	30.7	564	2	S76672
45	47	30.7	943	2	S44636

## ALIGNMENTS

### RESULT 1

ICHU2  
Interleukin-2 precursor [validated] - human  
A:Alternate names: IL-2; T-cell growth factor  
C:Species: Homo sapiens (man)  
C:Date: 11-Aug-1983 #sequence\_revision 11-Aug-1983 #text\_change 08-Dec-2000  
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;  
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.  
Nucleic Acids Res. 12, 5005-5013, 1984  
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo  
A:Reference number: A93524; MUID:84247353; PMID:6330695  
A:Accession: A01849  
A:Molecule type: DNA  
A:Residues: 1-153 <HO2>  
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2  
R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.  
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983  
A:Title: Structure of the human interleukin 2 gene.  
A:Reference number: A21192; MUID:84170243; PMID:6324170  
A:Accession: A21192  
A:Molecule type: DNA  
A:Residues: 1-153 <FU>  
A:Cross-references: GB:J00264; NID:g186294; PIDN:AAD48509.1; PID:g5729676  
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt  
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984  
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the g  
A:Reference number: A20961; MUID:84170356; PMID:6608729  
A:Accession: A20961  
A:Molecule type: DNA  
A:Residues: 1-153 <HO2>  
A:Cross-references: GB:K02056; NID:g186302; PIDN:AAA98792.1; PID:g386819  
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi  
EMBO J. 11, 3897-3904, 1992  
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t  
A:Reference number: S31208; MUID:93010984; PMID:1396583  
A:Accession: S31209  
A:Molecule type: mRNA  
A:Residues: 11-117 <LAA>  
A:Cross-references: EMBL:Z14955  
A:Note: this sequence is shown from the beginning of the fragment to the chromosomal  
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Ham  
Nature 302, 305-310, 1983  
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.  
A:Reference number: A93297; MUID:83167472; PMID:6403867  
A:Accession: A93297  
A:Molecule type: mRNA  
A:Residues: 1-153 <TAN>  
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781  
A:Experimental source: leukemic T-cell line, Jurkat-111, Cloned from Jurkat-FHCRC  
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K  
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983  
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840; PMID:6312994  
A:Accession: A90113  
A:Molecule type: mRNA  
A:Residues: 1-153 <NAE>  
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676  
A:Experimental source: tonsillar mononuclear cells  
R:Devois, R.; Platnick, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau  
Nucleic Acids Res. 11, 4307-4323, 1983  
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia  
A:Reference number: A93478; MUID:83246551; PMID:6306584  
A:Accession: A93478  
A:Molecule type: mRNA  
A:Residues: 1-153 <DEV>  
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781  
A:Experimental source: splenocytes  
R:Eizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.  
J. Neurochem. 64, 1928-1936, 1995  
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as  
A:Reference number: I56518; MUID:95239150; PMID:7722480  
A:Accession: I56518  
A:Molecule type: mRNA  
A:Status: translated from GB/EMBL/DBJ  
A:Residues: 1-152 <ETZ>  
A:Cross-references: GB:S77834; NID:g999000  
A:Accession: I73624  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 5-7, 'F', '9-17', 'P', '19-32', 'X', '34-45', 'X', '47-143 <RES>  
A:Cross-references: GB:S77835; NID:g999001; PIDN:RAD14264.1; PID:g4261964  
R:Nishino, N.; Obaru, K.; Maeda, S.; Shmada, K.; Onoue, K.  
Biomed. Res. 6, 197-205, 1985  
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.  
A:Reference number: I52528  
A:Accession: I52528  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-68 <RE>  
A:Cross-references: GB:M33199; NID:g186296; PIDN:AAA59139.1; PID:g553508  
R:Stebelnist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;  
Mol. Cell. Biol. 6, 3042-3049, 1986  
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and  
A:Reference number: I57603; MUID:87064618; PMID:3491296  
A:Accession: I57603  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-68 <RE3>  
A:Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509  
R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.  
Biochemistry 27, 6883-6892, 1988  
A:Title: Structure-activity relationships of recombinant human interleukin 2.  
A:Reference number: I52401; MUID:89062420; PMID:3264184  
A:Contents: recombinant IL-2 and mutants expressed in E. coli  
A:Accession: I52401  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 'M', '21-153 <REA>  
A:Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818  
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without  
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.  
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984  
A:Title: Amino acid sequence and post-translational modification of human interleukin 2.  
A:Reference number: A94009; MUID:85038540; PMID:6333684  
A:Accession: A94009  
A:Molecule type: protein  
A:Residues: 21-153 <ROB>  
A:Note: disulfide bonds and carbohydrate binding site were determined  
A:Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl  
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)  
R:Conradt, H.S.; Nimitz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.  
J. Biol. Chem. 264, 17368-17373, 1989  
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and  
de.  
A:Reference number: A34463; MUID:90008901; PMID:2793860

A:Accession: A34463  
A:Molecule type: protein  
A:Residues: 21-35 <CON>  
A:Note: the O-linked glycosylation site in recombinant material matched that from hum  
R:Grabenhorst, E.; Hofer, B.; Nimitz, M.; Jaeger, V.; Conradt, H.S.  
Eur. J. Biochem. 215, 189-197, 1993  
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro  
A:Reference number: S34052; MUID:93345493; PMID:8344280  
A:Contents: annotation; glycosylation of variant forms expressed in insect cells  
C:Genetics:  
A:Gene: GDB:IL2  
A:Cross-references: GDB:119344; OMIM:147680  
A:Map position: 4q26-4q27  
A:Introns: 49/3; 69/3; 117/3  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-153/Product: interleukin-2 #status experimental <IL2>  
F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:78-125/Disulfide bonds: #status experimental  
Query Match 96.1%; Score 147; DB 1; Length 153;  
Best Local Similarity 96.8%; Pred. No. 5.6e-14;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APTSSSTKTKTQLEHLLKLQMLINGINNY 31  
|||||  
Db 21 APTSSSTKTKTQLEHLLKLQMLINGINNY 51  
|||||  
RESULT 2  
ICG12  
Interleukin-2 precursor - common gibbon  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Hylobates lar (common gibbon, white-handed gibbon)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
C:Accession: A94067; A01849  
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre  
Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985  
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c  
A:Reference number: A94067; MUID:86042650; PMID:3877307  
A:Accession: A94067  
A:Molecule type: mRNA  
A:Residues: 1-153 <CHE>  
A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015  
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201  
A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-153/Product: interleukin-2 #status predicted <IL2>  
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F:78-125/Disulfide bonds: #status predicted  
Query Match 96.1%; Score 147; DB 1; Length 153;  
Best Local Similarity 96.8%; Pred. No. 5.6e-14;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APTSSSTKTKTQLEHLLKLQMLINGINNY 31  
|||||  
Db 21 APTSSSTKTKTQLEHLLKLQMLINGINNY 51  
|||||  
RESULT 3  
JN0698  
Interleukin 2 precursor - cat  
C:Species: Felis silvestris catus (domestic cat)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 16-Jul-1999  
C:Accession: JN0698  
R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.  
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993  
A:Title: Sequence and functional characterization of feline interleukin 2.  
A:Reference number: JN0698; MUID:93356765; PMID:8352761

A:Accession: JN0698  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-154 <CO2>  
A:CROSS-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314  
C:Superfamily: interleukin-2  
C:Keywords: growth factor

Query Match 69.9%; Score 107; DB 2; Length 154;  
Best Local Similarity 70.0%; Pred. No. 3.7e-08;  
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 30  
DB 21 APASSSTKETQQLLELLDLRLNGVNN 50

RESULT 4  
A31278  
interleukin-2 precursor - rat  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Apr-1989 #sequence\_revision 26-Apr-1989 #text\_change 16-Jul-1999  
C:Accession: A45882; A31278  
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.  
Immunogenetics 30, 145-147, 1989  
A:Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cDNA  
A:Reference number: A45882; MUID:89339608; PMID:2788130  
A:Accession: A45882  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <MCK>  
A:CROSS-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910  
C:Superfamily: interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 63.4%; Score 97; DB 2; Length 155;  
Best Local Similarity 64.5%; Pred. No. 1.1e-06;  
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 31  
DB 21 APTSSPAKETQQLLELLDLQLVLLRGIDNY 51

RESULT 5  
S16241  
interleukin-2 precursor - pig  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
C:Accession: S16241; S15473  
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.  
Biochim. Biophys. Acta 1089, 257-258, 1991  
A:Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.  
A:Reference number: S16241; MUID:91274360; PMID:2054386  
A:Accession: S16241  
A:Molecule type: mRNA  
A:Residues: 1-154 <GOO>  
A:CROSS-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992  
R:Lefevre, F.  
submitted to the EMBL Data Library, March 1991  
A:Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain reaction  
A:Reference number: S15473  
A:Accession: S15473  
A:Molecule type: mRNA  
A:Residues: 1-154 <LEP>  
A:CROSS-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069  
C:Superfamily: interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-154/Product: interleukin-2 #status predicted <MAT>

Query Match 62.7%; Score 96; DB 2; Length 154;  
Best Local Similarity 64.5%; Pred. No. 1.5e-06;  
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 31  
DB 21 APTSSSTKKTQLEHLLKQLMILNGINN 51

RESULT 6  
S33509  
interleukin-2 - Mongolian jird  
C:Species: Meriones unguiculatus (Mongolian jird)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S33509  
R:Mal, Z.; Klei, T.; Horohov, D.  
submitted to the EMBL Data Library, October 1992  
A:Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2  
A:Reference number: S33509  
A:Accession: S33509  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <MAT>  
A:CROSS-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638  
C:Superfamily: interleukin-2

Query Match 62.1%; Score 95; DB 2; Length 155;  
Best Local Similarity 64.5%; Pred. No. 2.1e-06;  
Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 31  
DB 21 APTSSPAKEAQYQLLELLDLQLLGRGINNY 51

RESULT 7  
S31391  
interleukin-2 precursor - horse  
C:Species: Equus caballus (domestic horse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S31391  
R:Tavernor, A.S.; Butcher, G.W.  
submitted to the EMBL Data Library, November 1992  
A:Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.  
A:Reference number: S31391  
A:Accession: S31391  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-149 <TAV>  
A:CROSS-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077  
C:Superfamily: interleukin-2

Query Match 55.6%; Score 85; DB 2; Length 149;  
Best Local Similarity 53.3%; Pred. No. 5.6e-05;  
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 30  
DB 21 APTSSSKRETQQLKQLMDLKLLEGVNN 50

RESULT 8  
S38662  
interleukin-2 - goat  
C:Species: Capra aegagrus hircus (domestic goat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S38662  
R:Rimstad, E.  
submitted to the EMBL Data Library, November 1993  
A:Description: The molecular cloning and expression of caprine interleukin 2.  
A:Reference number: S38662  
A:Accession: S38662  
A>Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-155 <RIM>  
A:Cross-references: EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g416003  
C:Superfamily: Interleukin-2

Query Match 47.1% Score 72; DB 2; Length 155;  
Best Local Similarity 50.0%; Pred. No. 0.0045;  
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLKLQMLINGINN 30  
||||||| |::: ||| ||::: | |  
Db 21 APTSSSGNTMKVKSLLLDQLLEKVKV 50

## RESULT 9

S11488  
Interleukin-2 precursor - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S11488; S13102; S15517  
R:Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.  
Nucleic Acids Res. 18, 5883, 1990  
A:Title: cDNA cloning of ovine interleukin 2 by PCR.  
A:Reference number: S11488; MUID:91016933; PMID:2216781  
A:Accession: S11488  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <GOO>  
A:Cross-references: EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282  
R:Scow, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R.  
Nucleic Acids Res. 18, 7175, 1990  
A:Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain reaction.  
A:Reference number: S13102; MUID:91088336; PMID:2263496  
A:Accession: S13102  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-5, 'L', '7', 155 <SEO>  
A:Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811  
R:Bujdosó, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.  
submitted to the EMBL Data Library, April 1991  
A:Reference number: S15517  
A:Accession: S15517  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 21-153 <BUJ>  
A:Cross-references: EMBL:X60148  
C:Superfamily: Interleukin-2

Query Match 47.1% Score 72; DB 2; Length 155;  
Best Local Similarity 50.0%; Pred. No. 0.0045;  
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLKLQMLINGINN 30  
||||||| |::: ||| ||::: | |  
Db 21 APTSSSGNTMKVKSLLLDQLLEKVKV 50

## RESULT 10

I45913  
Interleukin-2 precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Jul-1999  
C:Accession: I45913; S21470; S20761  
R:Carretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.; Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986  
A:Title: Cloning, sequence, and expression of bovine interleukin 2.  
A:Reference number: I45913; MUID:86205869; PMID:3517854  
A:Accession: I45913  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-155 <CER>  
A:Cross-references: GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205  
R:Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.

submitted to the EMBL Data Library, December 1989  
A:Reference number: S21470  
A:Accession: S21470  
A:Molecule type: DNA  
A:Residues: 1-22 <AN2>  
A:Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453  
C:Genetics:  
A:Gene: IL-2  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce

Query Match 47.1% Score 72; DB 2; Length 155;  
Best Local Similarity 50.0%; Pred. No. 0.0045;  
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLKLQMLINGINN 30  
||||||| |::: ||| ||::: | |  
Db 21 APTSSSGNTMKVKSLLLDQLLEKVKV 50

## RESULT 11

S37289  
Interleukin-2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S37289; S27205; S36162; S24936  
R:Todd, J.A.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S37289  
A:Accession: S37289  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-169 <TOD>  
A:Cross-references: EMBL:X73040  
R:Matesanz, F.; Aicini, A.; Pellicer, A.  
Biochim. Biophys. Acta 1132, 335-336, 1992  
A:Title: A new cDNA sequence for the murine interleukin-2 gene.  
A:Reference number: S27205; MUID:93041941; PMID:1420317  
A:Accession: S27205  
A:Molecule type: mRNA  
A:Residues: 1-63 <MATE>  
A:Cross-references: EMBL:X66058; NID:g52725; PIDN:CAA46854.1; PID:g52726  
R:Ghosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.  
Nature Genet. 4, 404-409, 1993  
A:Title: Polygenic control of autoimmune diabetes in nonobese diabetic mice.  
A:Reference number: S36162; MUID:94004970; PMID:8401590  
A:Accession: S36162  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-50 <GHO>  
A:Cross-references: EMBL:X73040  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-63/Product: interleukin-2 #status predicted <NAT>

Query Match 45.1% Score 69; DB 2; Length 169;  
Best Local Similarity 45.9%; Pred. No. 0.014;  
Matches 17; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 1 APTSSSTKKTQQLQ-----LEHLLKLQMLINGINN 31  
:|||||: |::: ||| ||::: | |  
Db 29 SPTSSSTAQAQQQQQQHLEQLLMDLQELLSRMENY 65

## RESULT 12

ICMS2  
Interleukin-2 precursor - mouse  
N:Alternate names: IL-2; T-cell growth factor (TCGF)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 21-Jul-2000  
C:Accession: A93550; A54490; A48597; I48590; I84713  
R:Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.



Nucleic Acids Res. 12, 9323-9331, 1984

A>Title: Organization and structure of the mouse interleukin-2 gene.

A:Reference number: A9350; MUID:85087940; PMID:6240025

A:Accession: A9350

A:Molecule type: DNA

A:Residues: 1-169 <FUS>

R:Degrave, W.; Simon, G.; Devos, R.; Plaetinck, G.; Tavernier, J.; Fiers, W. Mol. Biol. Rep. 11, 57-61, 1986

A>Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.

A:Reference number: A54490; MUID:86118396; PMID:3003564

A:Accession: A54490

A:Molecule type: DNA

A:Residues: 1-169 <DEG>

A:Cross-references: GB:M16760

R:Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K. Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985

A>Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clones

A:Reference number: A94064; MUID:85113172; PMID:3918306

A:Accession: A94064

A:Molecule type: mRNA

A:Residues: 1-169 <YOK>

A:Cross-references: GB:K02292; NID:g198330; PIDN:AAA39289.1; PID:g309404

R:Kashima, N.; Nishi-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Taniguchi Nature 313, 402-404, 1985

A>Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.

A:Reference number: I48597; MUID:85111148; PMID:2578624

A:Accession: I48597

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-169 <RES>

A:Cross-references: EMBL:X01772; GB:K02797; NID:g52663; PIDN:CAA25909.1; PID:g758159

C:Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this P

C:Genetics:

A: Introns: 63/3; 83/3; 132/3

C:Superfamily: Interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-169/Product: interleukin-2 #status predicted <MAT>

F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted

F:92-140/Disulfide bonds: #status predicted

Query Match 41.8%; Score 64; DB 1; Length 169;  
Best Local Similarity 37.8%; Pred. No. 0.072;  
Matches 17; Conservative 6; Mismatches 8; Indels 14; Gaps 1;

QY 1 APTSSST-----KKTQLQHLLKLQMLANGINNY 31  
||||||| : || ||| : | : |  
Db 21 APTSSSTSSSTAENAKQQQQQQQQQQHLEQLMDLQELLSRMENY 65

RESULT 13

H64307

C:Hypothetical protein MJ0064 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: H64307

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rsor, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.N.; Hurst, M.A. Science 273, 1098-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: H64307

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-189 <BUL>

A:Cross-references: GB:U67464; GB:L77117; NID:g1590852; PIDN:AAB98051.1; PID:g1590855;

C:Genetics:

A:Map position: FOR61888-62457

A:Start codon: GTG

Query Match 39.9%; Score 61; DB 2; Length 189;

Best Local Similarity 37.9%; Pred. No. 0.22;  
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 3 TSSSTKTKTQLEHLLKQLQMLNGINNY 31  
DB 22 SSSSVLETFEIVLDEIYTKLNLNLISEINNY 50

RESULT 14  
GNLJG4  
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey)  
N:Contains: endonuclease (EC 3.1.1.-); retropepsin (EC 3.4.23.16); RNA-directed DNA p  
C:Species: simian immunodeficiency virus, SIV  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 03-Jun-2002  
C:Accession: B30045  
R:Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Mikl, K.; Kitam  
Nature 333, 457-461, 1988  
A:Title: Sequence of simian immunodeficiency virus from African green monkey, a new m  
A:Reference number: A30045; MUID:88232906; PMID:3374586  
A:Accession: B30045  
A:Molecule type: DNA  
A:Residues: 1-1061 <FUK>  
A:Cross-references: EMBL:X07805; NID:g61748; PID:gl335593  
C:Comment: Specific enzymatic cleavages may yield mature proteins including protease,  
C:Genetics:  
A:Gene: pol  
C:Superfamily: pol polyprotein  
C:Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polypeptide; reve  
F:111-210/Product: retropepsin #status predicted <RFP>  
F:134/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 35.3%; Score 54; DB 1; Length 1061;  
Best Local Similarity 58.8%; Pred. No. 15;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 TQLEHLLKQLQMLN 26  
DB 976 TQLEHLLKQLQMLN 992

RESULT 15  
SL2169  
Isopenicillin N acyltransferase (EC 2.3.1.1) - Emericella nidulans  
N:Alternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltran  
C:Species: Emericella nidulans, Aspergillus nidulans  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: S12169; A36142; S09090  
R:Montenegro, E.; Barredo, J.L.; Gutierrez, S.; Diaz, B.; Alvarez, E.; Martin, J.F.  
Mol. Gen. Genet. 221, 322-330, 1990  
A:Title: Cloning, characterization of the acyl-CoA:6-amino penicillanic acid acyltran  
A:Reference number: S12169; MUID:90340281; PMID:2166227  
A:Accession: S12169  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <MON>  
A:Cross-references: EMBL:X53310; NID:g2378; PIDN:CAA37394.1; PID:g2379  
R:Tobin, M.B.; Fleming, M.D.; Skatrud, P.L.; Miller, J.R.  
J. Bacteriol. 172, 5908-5914, 1990  
A:Title: Molecular characterization of the acyl-coenzyme A:isopenicillin N acyltransf  
herichia coli.  
A:Reference number: A36142; MUID:91008967; PMID:2120195  
A:Accession: A36142  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <TOB>  
A:Cross-references: GB:M58293; NID:g167999; PIDN:AAA33287.1; PID:g168000  
R:Whitman, P.A.; Abraham, E.P.; Baldwin, J.E.; Fleming, M.D.; Schofield, C.J.; Suther  
FEBS Lett. 262, 342-344, 1990  
A:Title: Acyl coenzyme A: 6-aminopenicillanic acid acyltransferase from Penicillium c  
A:Reference number: S09089; MUID:90242961; PMID:2110531  
A:Accession: S09090  
A:Molecule type: protein  
A:Residues: 103-122 <WHI>

C;Genetics:  
A;Introns: 12/3; 71/1; 121/3  
C;Keywords: acyltransferase  
Query Match 34.6%; Score 53; DB 2; Length 357;  
Best Local Similarity 52.6%; Pred. No. 6.5;  
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
Qy 7 TTKTQLQLEHLLKIQMIL 25  
Db 40 TTKTQAELEQLLEQVM 58

Search completed: February 20, 2003, 10:07:25  
Job time : 29.0476 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:01:02 ; Search time 6.88889 Seconds  
(without alignments)  
186.643 Million cell updates/sec

Title: US-09-776-781-8

Perfect score: 153

Sequence: 1 APTSSSTKTKTQLQLHLLKLMILNINNY 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.1	153	1 IL2_HUMAN	P01585 homo sapien
2	147	96.1	154	1 IL2_MACFA	Q29615 macaca fasc
3	147	96.1	154	1 IL2_MACMU	P31498 macaca mula
4	142	92.8	154	1 IL2_CERTO	P46649 cercopithec
5	116	75.8	154	1 IL2_MIRAN	O62641 mirounga an
6	107.5	70.3	155	1 IL2_CANFA	Q29416 canis famil
7	107	69.9	153	1 IL2_RABIT	O77620 oryctolagus
8	107	69.9	154	1 IL2_FELCA	Q07885 felis silve
9	97	63.4	155	1 IL2_RAT	P17108 rattus norv
10	96	62.7	154	1 IL2_PIG	P26891 sus scrofa
11	95	62.1	155	1 IL2_MERUN	Q08081 meriones un
12	88	57.5	152	1 IL2_ORCOR	O97513 orcinus orc
13	85	55.6	149	1 IL2_HORSE	P37997 equus cabal
14	72	47.1	155	1 IL2_BOVIN	P05016 bos taurus
15	72	47.1	155	1 IL2_CAPHI	P36835 capra hircu
16	72	47.1	155	1 IL2_SHEEP	P19114 ovis aries
17	72	47.1	162	1 IL2_CEREL	P51747 cervus elap
18	64.5	42.2	166	1 IL2_MUSSP	Q08867 mus spretus
19	64	41.8	169	1 IL2_MOUSE	P04351 mus musculu
20	61	39.9	189	1 Y064_METJA	Q60376 methanococc
21	56	36.6	1046	1 POL_SIVAG	P27980 simian immu
22	54	35.3	1061	1 POL_SIVAT	P05895 simian immu
23	53	34.6	357	1 AAAA_EMENI	P21133 emericecella
24	51.5	33.7	415	1 CGA2_XENLA	P47827 xenopus lae
25	50.5	33.0	741	1 RN5A_HUMAN	Q05823 xenopus lae
26	48.5	31.7	452	1 TRPC_HELPY	Q25867 helicobacte
27	47.5	31.0	150	1 RNK6_SALIS	O46529 salmirmi sci
28	47.5	31.0	154	1 RNK6_BOVIN	P08904 bos taurus
29	47	30.7	257	1 ABCX_GALSU	P35020 galdieria s
30	47	30.7	406	1 CGA2_BOVIN	P30274 bos taurus
31	47	30.7	421	1 CGA1_MOUSE	Q61456 mus musculu
32	47	30.7	432	1 CGA2_HUMAN	P20248 homo sapien
33	47	30.7	465	1 CGA1_HUMAN	P78396 homo sapien

#### RESULT 1

ID	IL2_HUMAN	STANDARD;	PRT;	153 AA.
AC	P01585;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)			
DE	(Aldesleukin).			
GN	IL2.			
OS	Homo sapiens (Human), and			
OS	Hylobates lar (Common gibbon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606, 9580;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RC	MEDLINE=84247353; PubMed=6330695;			
RA	Holbrook N.J., Lieber M., Crabtree G.R.;			
RT	"DNA sequence of the 5' flanking region of the human interleukin 2 gene: homologues with adult T-cell leukemia virus.";			
RL	Nucleic Acids Res. 12:5005-5013(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RC	MEDLINE=83167472; PubMed=6403867;			
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,			
RA	Yoshimoto R., Hamuro J.;			
RT	"Structure and expression of a cloned cDNA for human interleukin-2.";			
RL	Nature 302:305-310(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RC	MEDLINE=84023840; PubMed=6312994;			
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,			
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;			
RT	"Cloning of interleukin 2 mRNAs from human tonsils.";			
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RC	MEDLINE=83245551; PubMed=6306584;			
RA	Devos R., Plaetinck G., Cheroutre H., Simons G., Degraeve W.,			
RA	Tavernier J., Remaut E., Fiers W.;			
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in E. coli.";			
RL	Nucleic Acids Res. 11:4307-4323(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RC	MEDLINE=84170356; PubMed=6608729;			
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,			
RA	Wiskocil R.L., Crabtree G.R.;			
RT	"T-cell growth factor: complete nucleotide sequence and organization of the gene in normal and malignant cells.";			

34 47 30.7 943 1 YLM5\_CABEL  
35 47 30.7 1492 1 CFTR\_SQUAC  
36 46.5 30.4 989 1 T100\_HUMAN  
37 46 30.1 532 1 G6PI\_BORBU  
38 46 30.1 746 1 PCAP\_HUMAN  
39 46 30.1 792 1 PCAP\_MOUSE  
40 45 29.4 81 1 LEU3\_PASMU  
41 45 29.4 368 1 LEU3\_NEUCR  
42 45 29.4 479 1 ZW10\_DROPS  
43 45 29.4 903 1 WSP1\_SCHPO  
44 45 29.4 1019 1 POLSIVSA  
45 45 29.4 1158 1 ALAL\_ARATH

#### ALIGNMENTS

P34408 caenorhabdi  
P26362 squalus aca  
O75448 homo sapien  
O51672 borrelia bu  
O96rn5 homo sapien  
Q224h2 mus musculu  
Q9cna0 pasteurella  
P34738 neurospora  
O44218 schizosacch  
P87320 schizosacch  
P12502 simian immu  
P98204 arabidopsis

RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=84170243; PubMed=63241170;  
RA Fujita T., Takosaka C., Matsui H., Taniguchi T.;  
RT "Structure of the human interleukin 2 gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=95239150; PubMed=7722480;  
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;  
RT "Interleukin-2 transcripts in human and rodent brains: possible  
expression by astrocytes.";  
RL J. Neurochem. 64:1928-1936(1995).  
RN [8]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human; TISSUE=Placenta;  
RX MEDLINE=96422299; PubMed=8824916;  
RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;  
RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:  
possible role in maintenance of fetal allograft.";  
RL Mol. Reprod. Dev. 43:180-186(1996).  
RN [9]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
Nickerson D.A.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 21-153 FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=89062420; PubMed=3264184;  
RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;  
RT "Structure-activity relationships of recombinant human interleukin  
2.";  
RL Biochemistry 27:6883-6892(1988).  
RN [11]  
RP SEQUENCE OF 1-69 FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=87064618; PubMed=3491296;  
RA Stebenliet U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,  
Ramoun M., Kant J.A., Crabtree G.R.;  
RT "Promoter region of interleukin-2 gene undergoes chromatin structure  
changes and confers inducibility on chloramphenicol acetyltransferase  
gene during activation of T cells.";  
RL Mol. Cell. Biol. 6:3042-3049(1986).  
RN [12]  
RP SEQUENCE OF 1-68 FROM N.A.  
RC SPECIES=Human;  
RA Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;  
RT "Organization of the DNA regions flanking the human interleukin 2  
gene.";  
RL Biomed. Res. 6:197-205(1985).  
RN [13]  
RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES=Human;  
RX MEDLINE=85038540; PubMed=6333684;  
RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;  
RT "Amino acid sequence and post-translational modification of human  
interleukin 2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).  
RN [14]  
RP CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES=Human;  
RX MEDLINE=9008901; PubMed=2793860;  
RA Conradt H.S., Nimtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,  
Hauser H.;  
RT "Expression of human interleukin-2 in recombinant baby hamster  
kidney, Ltk+, and Chinese hamster ovary cells. Structure of O-linked  
carbohydrate chains and their location within the polypeptide.";  
RL J. Biol. Chem. 264:17368-17373(1989).

RN [15]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=86042650; PubMed=3877307;  
RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,  
Greengard J.S., Crabtree G.R., Lin Y.;  
RT "A viral long terminal repeat in the interleukin 2 gene of a cell  
line that constitutively produces interleukin 2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RC SPECIES=Human;  
RX MEDLINE=88070646; PubMed=3500515;  
RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;  
RT "Three-dimensional structure of interleukin-2.";  
RL Science 238:1707-1709(1987).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=92335891; PubMed=1631562;  
RA Bazan J.F.;  
RT "Unraveling the structure of IL-2.";  
RL Science 257:410-412(1992).  
RN [18]  
RP RESPONSE TO ABOVE LETTER.  
RA McKay D.B.;  
RL Science 257:412-413(1992).  
RN [19]  
RP STRUCTURE BY NMR.  
RX MEDLINE=92379010; PubMed=1510960;  
RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,  
Campbell I.D.;  
RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR  
experiments.";  
RL Biochemistry 31:7741-7744(1992).  
RN [20]  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE=95111955; PubMed=7529123;  
RA Bamorough P., Hedgecock C.J., Richards W.G.;  
RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
modelling.";  
RL Structure 2:839-851(1994).  
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS  
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)  
WHICH INVOLVES IL2 AND BCMA.  
CC -!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used  
in patients with renal cell carcinoma or metastatic melanoma.  
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
CC -!- DATABASE: NAME-R&D Systems' cytokine source book: IL2;  
WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyid=206".  
-----  
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-----  
CC EMBL; J00264; A048509.1; -  
DR EMBL; X01586; CAA25742.1; -  
DR EMBL; V00564; CAA23827.1; -  
DR EMBL; X00695; CAA25292.1; -  
DR EMBL; K02056; AAA98792.1; -  
DR EMBL; M13879; AAA59141.1; -  
DR EMBL; K03174; AAA35453.1; -  
DR EMBL; S77834; AAD14263.2; -  
DR EMBL; S82692; AAB46883.1; -

Query Match 96.1%; Score 147; DB 1; Length 153;  
 Best Local Similarity 96.8%; Pred. No. 4.3e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLKLLQMLNGINNY 31  
 DB 21 APTSSSTKTKTQLEHLKLLQMLNGINNY 51

## RESULT 2

## IL2\_MACFA

ID IL2\_MACFA STANDARD; PRT; 154 AA.  
 AC Q29615;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE-Peripheral blood;

RA Yabe M., Matsura Y., Tatsumi M.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY  
 CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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CC -----  
 CC EMBL; D63352; BAA09676.1; -;  
 CC HSSP; P01585; 3INK.

CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam: PF00715; IL2; 1.

CC PRINTS; PR00265; INTERLEUKIN2.  
 CC ProDom; PD003649; Interleukin-2; 1.

CC SMART; SM00189; IL2; 1.  
 CC PROSITE; PS00424; INTERLEUKIN\_2; 1.

CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 154 INTERLEUKIN-2.

FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.

FT SEQUENCE 154 AA; 17686 MW; 7853FE62A5E4A49 CRC64;  
 SQ

Query Match 96.1%; Score 147; DB 1; Length 154;  
 Best Local Similarity 96.8%; Pred. No. 4.3e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLKLLQMLNGINNY 31  
 DB 21 APTSSSTKTKTQLEHLKLLQMLNGINNY 51

## RESULT 3

## IL2\_MACMU

ID IL2\_MACMU STANDARD; PRT; 154 AA.  
 AC P51498;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.

OS Macaca mulatta (Rhesus macaque), and  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9544, 9545;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood;  
 RX MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 nonhuman primates.";  
 RL J. Immunol. 155:3946-3954(1995).

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY  
 CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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CC -----  
 CC EMBL; U19847; AAB60400.1; -;  
 CC EMBL; U19852; AAA86714.1; -;  
 CC HSSP; P01585; 3INK.

CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam: PF00715; IL2; 1.

CC PRINTS; PR00265; INTERLEUKIN2.  
 CC ProDom; PD003649; Interleukin-2; 1.

CC SMART; SM00189; IL2; 1.  
 CC PROSITE; PS00424; INTERLEUKIN\_2; 1.

CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 154 INTERLEUKIN-2.

FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.

FT SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;  
 SQ

Query Match 96.1%; Score 147; DB 1; Length 154;  
 Best Local Similarity 96.8%; Pred. No. 4.3e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLKLLQMLNGINNY 31  
 DB 21 APTSSSTKTKTQLEHLKLLQMLNGINNY 51

RESULT 4  
 IL2\_CERTO  
 ID IL2\_CERTO STANDARD; PRT; 154 AA.  
 AC P46649;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.

OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecinae; Cercocebus.  
 CC NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 nonhuman primates.";  
 RL J. Immunol. 155:3946-3954(1995).  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL  
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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 CC -----  
 CC EMBL; U19846; AAB60399.1; -.  
 DR HSP; P01585; 3INK.  
 DR InterPro: IPR000779; Interleukin-2.  
 DR Pfam: PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR PRODOM; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 T-cell.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 154 INTERLEUKIN-2.  
 FT CARBOHYD 23 23 O-LINKED (GALNAc... ) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.  
 FT VARIANT 25 25 R -> S.  
 FT VARIANT 74 74 K -> E.  
 SQ SEQUENCE 154 AA; 17754 MW; 9FEB51814204BA48 CRC64;  
 Query Match 92.8%; Score 142; DB 1; Length 154;  
 Best Local Similarity 93.5%; Pred. No. 2.4e-14;  
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 APTSSSTKKTQLEHLLKLQMLINGNNY 31  
 |||||  
 Db 21 APTSSSTKKTQLEHLLKLQMLINGNNY 51  
 RESULT 5  
 IL2\_MIRAN  
 ID IL2\_MIRAN STANDARD; PRT; 154 AA.  
 AC O62641;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Mirounga angustirostris (Northern elephant seal).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.  
 CC NCBI\_TaxID=9716;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98136705; PubMed=9476229;  
 RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;

RT "Sequence and characterization of phocine interleukin 2.";  
 RL Wildl. Dis. 34:81-90(1998).  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL  
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY  
 SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U79187; AAC12258.1; -.  
 DR HSP; P01585; 3INK.  
 DR InterPro: IPR000779; Interleukin-2.  
 DR Pfam: PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR PRODOM; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 T-cell.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 154 INTERLEUKIN-2.  
 FT CARBOHYD 23 23 O-LINKED (GALNAc... ) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.  
 SQ SEQUENCE 154 AA; 17661 MW; 0C923337A4B16B6BB CRC64;  
 Query Match 75.8%; Score 116; DB 1; Length 154;  
 Best Local Similarity 71.0%; Pred. No. 2.1e-10;  
 Matches 22; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 APTSSSTKKTQLEHLLKLQMLINGNNY 31  
 |||||  
 Db 21 APTSSSTKKTQLEHLLKLQMLINGNNY 51  
 RESULT 6  
 IL2\_CANFA  
 ID IL2\_CANFA STANDARD; PRT; 155 AA.  
 AC Q29416; Q28249;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 CC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=XBRED21/12/93; TISSUE=Lymph node;  
 RX MEDLINE=95337423; PubMed=7612930;  
 RA Dunham S.P., Argyle D.J., Onions D.E.;  
 RT "The isolation and sequence of canine interleukin-2.";  
 RL DNA Seq. 5:177-180(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96016696; PubMed=8571541;  
 RA Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,  
 Henthorn P.S.;  
 RT "A single nucleotide insertion in the canine interleukin-2 receptor  
 gamma chain results in X-linked severe combined immunodeficiency  
 disease.";  
 RL Vet. Immunol. Immunopathol. 47:203-213(1995).



CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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 CC -----  
 CC EMBL; L19402; AAA02865.1; -  
 CC EMBL; L25408; AAA51431.1; -  
 CC PIR; JN0598; JN0698.  
 CC HSSP; P01585; 3INK.  
 CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam; PF00715; IL2; 1.  
 CC PRINTS; PD0265; INTERLEUKIN2.  
 CC PRODOM; PD003649; Interleukin-2; 1.  
 CC SMART; SM00189; IL2; 1.  
 CC PROSITE; PS00424; INTERLEUKIN2; 1.  
 CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 CC T-cell.  
 CC SIGNAL 1 20 BY SIMILARITY.  
 CC CHAIN 21 154 INTERLEUKIN-2.  
 CC DISULFID 78 126 BY SIMILARITY.  
 CC CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CONFLICT 3 4 KI -> RM (IN REF. 2).  
 CC CONFLICT 150 150 F -> I (IN REF. 2).  
 CC SEQUENCE 154 AA; 17653 MW; 2E71E3BD8B9665EF CRC64;  
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 CC Query Match 69.9%; Score 107; DB 1; Length 154;  
 CC Best Local Similarity 70.0%; Pred. No. 4.7e-09;  
 CC Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 CC  
 CC QY 1 APTSSSTKTKTQLEHLLKLMILNGINN 30  
 CC || |||||:| | | | | :| | | | |  
 CC DB 21 APASSSTKETQQLLEQLLDRLLLNGVN 50  
 CC  
 CC RESULT 9  
 CC IL2\_RAT  
 CC ID IL2\_RAT STANDARD; PRT; 155 AA.  
 CC AC P17108;  
 CC DT 01-AUG-1990 (Rel. 15, Created)  
 CC DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 CC GN IL2 OR IL-2.  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 CC OX NCBI\_TaxID=10116;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=89339608; PubMed=2788130;  
 CC RA McKnight A.J., Mason D.W., Barclay A.N.;  
 CC RT "Sequence of rat interleukin 2 and anomalous binding of a mouse  
 CC RT interleukin 2 CDNA probe to rat MHC class II-associated invariant  
 CC RT chain mRNA";  
 CC RL Immunogenetics 30:145-147(1989).  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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 CC -----  
 CC EMBL; M22899; AAA41427.1; -  
 CC PIR; A31278; A31278.  
 CC PIR; A45882; A45882.  
 CC HSSP; P01585; 3INK.  
 CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam; PF00715; IL2; 1.  
 CC PRINTS; PD0265; INTERLEUKIN2.  
 CC PRODOM; PD003649; Interleukin-2; 1.  
 CC SMART; SM00189; IL2; 1.  
 CC PROSITE; PS00424; INTERLEUKIN2; 1.  
 CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 CC T-cell.  
 CC SIGNAL 1 20 BY SIMILARITY.  
 CC CHAIN 21 155 INTERLEUKIN-2.  
 CC CARBOHYD 23 23 O-LINKED (GALNAC. .) (BY SIMILARITY).  
 CC DISULFID 78 126 BY SIMILARITY.  
 CC SEQUENCE 155 AA; 17632 MW; 67A8554A73BF30A0 CRC64;  
 CC  
 CC Query Match 63.4%; Score 97; DB 1; Length 155;  
 CC Best Local Similarity 64.5%; Pred. No. 1.5e-07;  
 CC Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 CC  
 CC QY 1 APTSSSTKTKTQLEHLLKLMILNGINN 31  
 CC |||||:| | | | | :| | | | |  
 CC DB 21 APTSSPAKETQQLLEQLLDQLVLLRGIDNY 51  
 CC  
 CC RESULT 10  
 CC IL2\_PIG  
 CC ID IL2\_PIG STANDARD; PRT; 154 AA.  
 CC AC P26891;  
 CC DT 01-AUG-1992 (Rel. 23, Created)  
 CC DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 CC GN IL2.  
 CC OS Sus scrofa (Pig).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CC OX NCBI\_TaxID=9823;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=T-cell;  
 CC RX MEDLINE=91274360; PubMed=2054386;  
 CC RA Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;  
 CC RT "CDNA cloning of porcine interleukin 2 by polymerase chain reaction.";  
 CC RL Biochim. Biophys. Acta 1089:257-258(1991).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=T-cell;  
 CC RA Lefevre F.;  
 CC RT Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.  
 CC RN [3]  
 CC RP SEQUENCE FROM N.A.  
 CC RA Iwata H., Hasegawa A., Yamamoto M., Oida T., Endo Y., Inoue T.;  
 CC RT "Structure of the porcine chromosomal interleukin-2 gene";  
 CC RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
KW T-cell.

CC	or send an email to <a href="mailto:license@sb-sib.ch">license@sb-sib.ch</a> .
CC	-----
CC	EMBL; X68779; CAA48679.1; -
DR	-----

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FT CONFLICT      8      S -> A (IN REF. 2).
FT CONFLICT     59      I -> M (IN REF. 2).
FT CONFLICT    125     N -> D (IN REF. 2).
FT CONFLICT    128     E -> G (IN REF. 2).
FT CONFLICT    145     I -> F (IN REF. 2).
FT CONFLICT    148     L -> M (IN REF. 2).
SQ SEQUENCE    149 AA; 17086 MW;  051BB8C47A0114FC CRC64;

Query Match      55.6%; Score 85; DB 1; Length 149;
Best Local Similarity 53.3%; Pred. No. 9,4e-06;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gap

QY 1 APTSSSTKTKTQLEHLLKLQMLINGINN 30
      ||||| :||| ||: | :||| :|||
Db 21 APTSSSKRETQOQLQQLMDLKLLEGVNN 50

RESULT 14
IL2_BOVIN
ID IL2_BOVIN STANDARD; PRT; 155 AA.
AC P05016;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2 OR IL-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX 11
SEQUENCE FROM N.A.
RP RP MEDLINE=86205869; PubMed=3517854;
RX Carretti D.P., McKersghan K., Larsen A., Cantrell M.A., Anderson D.
RA Gyllis S., Cosman D., Baker P.E.;
RT "Cloning, sequence, and expression of bovine Interleukin 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
RN [2]
RP RP SEQUENCE FROM N.A.
RX MEDLINE=86205870; PubMed=3486415;
RA Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,
RT Barr P.J., Magnuson N.S., Magnuson J.A.;
RN "Molecular cloning of a functional bovine Interleukin 2 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
RN [3]
RP RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Thymus;
RC Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC EMBL; M12791; AAA30586.1; -
CC DR EMBL; M13204; AAA21143.1; ALT_INIT.
CC DR EMBL; X17201; CAA35062.1; -
CC DR EMBL; X52687; CAA36912.1; -
CC DR HSSP; P01585; 3INK.
CC DR DR InterPro; IPR000779; Interleukin-2.
CC DR Pfam; PF00715; IL2; 1.

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DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT DISULFID 79 127 BY SIMILARITY.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CONFLICT 66 66 V -> A (IN REF. 2).
SQ SEQUENCE 155 AA; 17627 MW; 816667DFEA052EDF CRC64;

Query Match 47.1%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0009;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLKQLQMLNGINN 30
DB 21 APTSSSTGNTMKVKSLLDLQLLEKVN 50

RESULT 15
IL2_CAPHI STANDARD; PRT; 155 AA.
AC P36835; P79156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rimstad E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beyer J.C.; Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
DR EMBL; X76063; CAA53664.1; -.
DR EMBL; U34274; AAB38527.1; -.
DR PIR; S38662; S38662.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.

```

```

FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 79 127 BY SIMILARITY.
FT CONFLICT 3 5 RMQ -> QIP (IN REF. 2).
FT CONFLICT 22 22 P -> T (IN REF. 2).
FT CONFLICT 30 30 T -> P (IN REF. 2).
FT CONFLICT 51 51 L -> P (IN REF. 2).
FT CONFLICT 71 71 D -> A (IN REF. 2).
FT CONFLICT 89 89 D -> E (IN REF. 2).
FT CONFLICT 99 99 R -> L (IN REF. 2).
FT CONFLICT 107 113 YMASLKG -> SMDNIKR (IN REF. 2).
FT CONFLICT 140 140 Q -> L (IN REF. 2).
FT CONFLICT 144 144 T -> I (IN REF. 2).
FT CONFLICT 154 154 L -> M (IN REF. 2).
SQ SEQUENCE 155 AA; 17703 MW; 90022DFBB6AF78DE CRC64;

Query Match 47.1%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0009;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLKQLQMLNGINN 30
DB 21 APTSSSTGNTMKVKSLLDLQLLEKVN 50

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Search completed: February 20, 2003, 10:05:24  
Job time : 6.88889 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:07 ; Search time 24.1111 Seconds  
(without alignments)  
264.918 Million cell updates/sec

Title: US-09-776-781-8  
Perfect score: 153  
Sequence: 1 APTSSSTKTKTQLEHLLKQLMILNGINNY 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP TREMBL\_21.\*
- 2: sp\_archaea.\*
- 3: sp\_bacteria.\*
- 4: sp\_fungi.\*
- 5: sp\_human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mammal.\*
- 8: sp\_mhc.\*
- 9: sp\_organelle.\*
- 10: sp\_phage.\*
- 11: sp\_plant.\*
- 12: sp\_rodent.\*
- 13: sp\_virus.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	147	96.1	150	4	Q9C001	Q9C001 homo sapien
2	145	94.8	154	6	Q9XS38	Q9XS38 papio hamad
3	135.5	88.6	156	4	Q13169	Q13169 homo sapien
4	134	87.6	139	4	Q16334	Q16334 homo sapien
5	108.5	70.9	155	6	Q9XT83	Q9XT83 halichoerus
6	107.5	70.3	66	6	Q9BG74	Q9BG74 canis famil
7	107	69.9	75	6	Q9TV12	Q9TV12 canis famil
8	106	69.3	155	11	Q923T2	Q923T2 sigmodon hi
9	103	67.3	138	11	Q70329	Q70329 mesocricetu
10	99	64.7	133	6	Q9WZ99	Q9WZ99 oryctolagus
11	84	54.9	23	4	Q9UCF5	Q9UCF5 homo sapien
12	78	51.0	154	6	Q9XT84	Q9XT84 delphinapte
13	75	49.0	152	11	Q88210	Q88210 cavia porce
14	72	47.1	69	6	Q9GJRA	Q9GJRA ovis aries
15	72	47.1	155	6	Q9GL83	Q9GL83 capra hircu
16	72	47.1	155	6	Q95KP3	Q95KP3 bubalus bub

17	69	45.1	39	6	Q9BG73	Q9BG73 canis famil
18	69	45.1	150	11	P70291	P70291 mus musculu
19	69	45.1	169	11	Q9QUS8	Q9QUS8 mus musculu
20	67	43.8	150	11	P70294	P70294 mus musculu
21	62.5	40.8	159	11	P70293	P70293 mus musculu
22	60.5	39.5	155	11	P70292	P70292 mus musculu
23	56	36.6	300	2	Q8VW37	Q8VW37 coxiella bu
24	56	36.6	348	12	Q9DHS6	Q9DHS6 yaba-like d
25	53	34.6	251	12	Q9PYU2	Q9PYU2 xestia c-ni
26	53	34.6	452	10	Q9ZV75	Q9ZV75 arabidopsi
27	52	34.0	116	6	Q29138	Q29138 trichechus
28	52	34.0	478	17	Q8TLR6	Q8TLR6 methanosarc
29	51	33.3	517	16	Q8R628	Q8R628 thermoanaer
30	51	33.3	737	16	Q9KTG5	Q9KTG5 vibrio chol
31	51	33.3	866	16	Q25517	Q25517 helicobacte
32	51	33.3	875	16	Q9ZK28	Q9ZK28 helicobacte
33	50	32.7	95	2	Q9F8U6	Q9F8U6 streptomyce
34	50	32.7	304	16	Q930K5	Q930K5 rhizobium m
35	50	32.7	543	16	Q9KSF8	Q9KSF8 vibrio chol
36	49.5	32.4	104	10	Q9FSQ4	Q9FSQ4 oryza sativ
37	49.5	32.4	367	10	Q9SIF5	Q9SIF5 arabidopsi
38	49.5	32.4	474	10	Q06376	Q06376 brassica na
39	49	32.0	145	16	Q9KAW0	Q9KAW0 bacillus ha
40	48.5	31.7	366	16	Q98G42	Q98G42 rhizobium l
41	48	31.4	311	16	Q9CLL6	Q9CLL6 pasteurella
42	48	31.4	398	16	Q50911	Q50911 borrelia bu
43	48	31.4	441	16	Q928V0	Q928V0 listeria in
44	48	31.4	441	16	Q69192	Q69192 listeria mo
45	48	31.4	765	16	P74599	P74599 synechocyst

#### ALIGNMENTS

##### RESULT 1

Q9C001 PRELIMINARY; PRT; 150 AA.  
AC Q9C001;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Interleukin-2 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20545237; PubMed=11093171;  
RA Matesanz F., Delgado C., Fresno M., Alcina A.;  
RT "Allelic selection of human IL-2 gene."  
RL Eur. J. Immunol. 30:3516-3521(2000).  
DR EMBL; AF228636; AAG53575.1; -  
DR HSP; P01585; 3INK  
DR InterPro; IPR000779; Interleukin-2.  
DR Pfam; PF00715; IL2; 1.  
DR PRINTS; PD00265; INTERLEUKIN2.  
DR ProDom; PD003649; Interleukin-2; 1.  
DR PROSITE; PS00189; IL2; 1.  
DR SMART; SM00189; IL2; 1.  
FT PROSITE; PS00424; INTERLEUKIN\_2; 1.  
FT NON\_TER 150 150  
SQ SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;

Query Match 96.1%; Score 147; DB 4; Length 150;

Best Local Similarity 96.8%; Pred. No. 4.3e-14;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKQLMILNGINNY 31

Db 21 APTSSSTKTKTQLEHLLKQLMILNGINNY 51

##### RESULT 2

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Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Actus lemurius (Northern gray-necked night monkey),
OS Actus nancyanae (Owl monkey),
OS Actus nigriceps (black-headed night monkey), and
OS Actus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RN SEQUENCE FROM N.A.
RP Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patatroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -
DR EMBL; U88364; AAD41534.1; -
DR EMBL; U88361; AAD41535.1; -
DR EMBL; U88363; AAD41536.1; -
DR EMBL; U88362; AAD41537.1; -
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 94.8%; Score 145; DB 6; Length 154;
Best Local Similarity 93.5%; Pred. No. 8.7e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
|||||
Db 21 APTSSSTKKTQLQLEHLLKLQMLINGINNY 51

RESULT 3
Q13169
ID Q13169 PRELIMINARY; PRT; 156 AA.
AC Q13169;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RA "Expression of human IL-2 from gene transferred mouse melanoma cells
RT and its effect on the growth of mouse melanoma.";
RL Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RN SEQUENCE FROM N.A.
RP Xu L.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U25676; AAA70092.1; -
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.

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DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B36389 CRC64;

Query Match 88.6%; Score 135.5; DB 4; Length 156;
Best Local Similarity 88.2%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 APTSSS---FKKTLQLEHLLKLQMLINGINNY 31
|||||
Db 21 APTSSSTKKTQLQLEHLLKLQMLINGINNY 54

RESULT 4
Q16334
ID Q16334 PRELIMINARY; PRT; 139 AA.
AC Q16334;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-95239150; PubMed-7722480;
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 87.6%; Score 134; DB 4; Length 139;
Best Local Similarity 90.3%; Pred. No. 3.5e-12;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
|||||
Db 17 APTSSSTKKTQLQLEHLLKLQMLINGINNY 47

RESULT 5
Q9XT83
ID Q9XT83 PRELIMINARY; PRT; 155 AA.
AC Q9XT83;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-99221046; PubMed-10206205;
RA St-Laurent G., Belliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";

```



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RC TISSUE=SPLEEN;
RX MEDLINE=98233044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046212; AAC40097.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match 67.3%; Score 103; DB 11; Length 138;
Best Local Similarity 71.0%; Pred. No. 1.5e-07;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
Db 14 APTSSSKETQQLQLQLDLQLQLKGINNY 44

RESULT 10
Q9WZ99 PRELIMINARY; PRT; 133 AA.
AC Q9WZ99;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 2 variant IL2delta2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, AND LYMPH NODE;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF169168; AAF86652.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 64.7%; Score 99; DB 6; Length 133;
Best Local Similarity 69.0%; Pred. No. 5.6e-07;
Matches 20; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLMILNGIN 29
Db 21 APTSSSTKETQQLDLQLDLQLKGVN 49

RESULT 11
Q9UCF5 PRELIMINARY; PRT; 23 AA.
ID Q9UCF5
AC Q9UCF5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Interleukin 13 precursor.
OS Cavia porcellus (Guinea pig).

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93289963; PubMed=8512072;
RA Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 54.9%; Score 84; DB 4; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TSSSTKKTQLQLEHLLKQLM 23
Db 3 TSXSTKKTQLQLEHLLKQLM 23

RESULT 12
Q9XT84 PRELIMINARY; PRT; 154 AA.
ID Q9XT84
AC Q9XT84;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 2.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Belliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RL 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072870; AAD40847.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 51.0%; Score 78; DB 6; Length 154;
Best Local Similarity 51.6%; Pred. No. 0.00087;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
Db 21 APTSSSTENTKKVQSLLQLDLHLKLNH 51

RESULT 13
O88210 PRELIMINARY; PRT; 152 AA.
ID O88210
AC O88210;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).
```



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RESULT 15
Q9GL83
ID Q9GL83 PRELIMINARY; PRT; 155 AA.
AC Q9GL83;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2.
DN IL-2.
GN IL-2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
OX [1]
RN SEQUENCE FROM N.A.
RA Ying Q.H., Li X.R., Pan J.Y.;
RT "Cloning of the goat IL-2 gene and its expression in E.coli.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307018; AAG28783.1; -.
DR HSP; P01585; 3INK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR SQ SEQUENCE 155 AA; EEB2DE18F5469AA CRC64;

Query Match 47.1%; Score 72; DB 6; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0069;
Matches 15; Conservative 6; Mismatches 9; Indels 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGNN 30
DB 21 APTSSSTGNTMKVAKSLLDLQLLLGKVN 50

Search completed: February 20, 2003, 10:06:22
Job time : 25.1111 secs

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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:04:02 ; Search time 19.1905 Seconds  
(without alignments)  
47.529 Million cell updates/sec

Title: US-09-776-781-8  
Perfect score: 153  
Sequence: 1 APTSSSTKTKTQLEHLLKLQMLNGINNY 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents:AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.1	50	1	US-08-127-351-13
2	147	96.1	50	1	US-08-480-3678-13
3	147	96.1	50	1	US-08-487-221A-13
4	147	96.1	50	1	US-08-480-370-13
5	147	96.1	88	4	US-08-817-787-15
6	147	96.1	96	1	US-08-160-376A-5
7	147	96.1	96	1	US-08-389-487-8
8	147	96.1	133	1	US-07-800-366-1
9	147	96.1	133	1	US-08-354-456A-5
10	147	96.1	133	1	US-08-225-224-3
11	147	96.1	133	1	US-08-318-193-89
12	147	96.1	133	1	US-08-284-393B-1
13	147	96.1	133	1	US-08-284-393B-2
14	147	96.1	133	1	US-08-284-393B-3
15	147	96.1	133	1	US-08-734-471-1
16	147	96.1	133	3	US-08-722-258-3
17	147	96.1	133	4	US-08-817-787-13
18	147	96.1	133	4	US-07-310-026-1
19	147	96.1	133	5	PCT-US95-04468-3
20	147	96.1	133	5	PCT-US95-08950-1
21	147	96.1	133	5	PCT-US95-08950-2
22	147	96.1	133	5	PCT-US95-08950-3
23	147	96.1	133	6	5210029-1
24	147	96.1	133	6	5256769-1
25	147	96.1	133	6	5464939-2
26	147	96.1	134	6	5496924-55
27	147	96.1	153	3	US-09-012-366-3

28	147	96.1	153	4	US-08-759-628-8	Sequence 8, Appl1
29	147	96.1	153	4	US-09-522-217-111	Sequence 111, App
30	147	96.1	153	6	5314995-7	Patent No. 5314995
31	147	96.1	157	4	US-08-818-562-2	Sequence 2, Appl1
32	147	96.1	157	4	US-09-628-445-2	Sequence 2, Appl1
33	147	96.1	478	3	US-08-155-888-2	Sequence 2, Appl1
34	147	96.1	504	1	US-07-932-915-2	Sequence 2, Appl1
35	147	96.1	504	5	PCT-US91-05826-2	Sequence 2, Appl1
36	144	94.1	251	3	US-08-875-811-59	Sequence 59, Appl
37	144	94.1	254	3	US-08-875-811-61	Sequence 61, Appl
38	143	93.5	133	1	US-08-354-456A-6	Sequence 6, Appl1
39	140	91.5	31	4	US-09-116-594-2	Sequence 3, Appl1
40	132.5	86.6	127	3	US-08-806-121B-3	Sequence 3, Appl1
41	132.5	86.6	127	4	US-09-443-061-3	Sequence 3, Appl1
42	96	62.7	21	4	US-09-570-921-63	Sequence 63, Appl
43	96	62.7	21	4	US-09-570-921-68	Sequence 68, Appl
44	95	62.1	141	4	US-08-930-917A-18	Sequence 18, Appl
45	72	47.1	135	2	US-08-383-621-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1  
US-08-127-351-13  
; Sequence 13, Application US/08127351  
; Patent No. 5449761  
; GENERAL INFORMATION:  
; APPLICANT: BELINKA JR, BENJAMIN A.  
; APPLICANT: COUGHLIN, DANIEL J.  
; APPLICANT: ALVAREZ, VERNON L.  
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATIER &  
; ADDRESSEE: NEUSTADT,  
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,351  
; FILING DATE: 28-SEP-1993  
; CLASSIFICATION: 53A  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-004-44  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-127-351-13

Query Match 96.1%; Score 147; DB 1; Length 50;  
Best Local Similarity 96.8%; Pred. No. 1.1e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

: GENERAL INFORMATION:
: APPLICANT: BELINKA, JR, BENJAMIN A.
: APPLICANT: COUGHLIN, DANIEL J.
: APPLICANT: ALVAREZ, VERNON L.
: APPLICANT: WOOD, RICHARD
: TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
: TITLE OF INVENTION: CONSTRUCTS
: NUMBER OF SEQUENCES: 56
: CORRESPONDENCE ADDRESS:
: ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER &
: ADDRESSER: NEUSTADT, P.C.

```

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/127,351  
 FILING DATE: 28-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Villacorta, Gilberto M.  
 REGISTRATION NUMBER: 34,038  
 REFERENCE/DOCKET NUMBER: 4980-004-44  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELE: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-480-370-13

Query Match 96.1%; Score 147; DB 1; Length 50;  
 Best Local Similarity 96.8%; Pred. No. 1.1e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLQLEHLLKQLMILGINNY 31  
 DB 1 APTSSSTKKTQLQLEHLLKQLMILGINNY 31

RESULT 5  
 US-08-817-787-15  
 Sequence 15, Application US/08817787  
 Patent No. 6294353  
 GENERAL INFORMATION:  
 APPLICANT: Pack, Peter  
 APPLICANT: Lupas, Andrei  
 TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF  
 TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FISH & NEAVE  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10020

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/817,787  
 FILING DATE: 23-SEP-1997  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP95/04117  
 FILING DATE:  
 PRIOR APPLICATION NUMBER: EP 94 11 6558.1  
 APPLICATION NUMBER:  
 FILING DATE: 20-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 88 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-817-787-15

Query Match 96.1%; Score 147; DB 4; Length 88;  
 Best Local Similarity 96.8%; Pred. No. 2.2e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLQLEHLLKQLMILGINNY 31  
 DB 3 APTSSSTKKTQLQLEHLLKQLMILGINNY 33

RESULT 6  
 US-08-160-376A-5  
 Sequence 5, Application US/08160376A  
 Patent No. 5473049  
 GENERAL INFORMATION:  
 APPLICANT: Obermeier, Ranier  
 APPLICANT: Gerl, Martin  
 APPLICANT: Ludwig, Jurgen  
 APPLICANT: Sabel, Walter  
 TITLE OF INVENTION: Process For Obtaining Proinsulin  
 TITLE OF INVENTION: Possessing Correctly Linked  
 TITLE OF INVENTION: Cystine Bridges  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kenneth A. Genoni, Esq.  
 STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500  
 CITY: Somerville  
 STATE: New Jersey  
 COUNTRY: U.S.A.  
 ZIP: 08876-1258  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
 COMPUTER: IBM 386  
 OPERATING SYSTEM: WINDOWS 3.1  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/160,376A  
 FILING DATE: December 1, 1993  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GE P 4240420.7  
 FILING DATE: December 2, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barbara V. Maurer, Esq.  
 REGISTRATION NUMBER: 31,287  
 REFERENCE/DOCKET NUMBER: HOE 92/F 384  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 231-4079  
 TELEFAX: (908) 231-2255  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 Amino Acids  
 TYPE: Amino Acid (AA)  
 TOPOLOGY: not relevant  
 US-08-160-376A-5

Query Match 96.1%; Score 147; DB 1; Length 96;  
 Best Local Similarity 96.8%; Pred. No. 2.4e-15;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLQLEHLLKQLMILGINNY 31  
 DB 2 APTSSSTKKTQLQLEHLLKQLMILGINNY 32

RESULT 7  
 US-08-389-487-8  
 Sequence 8, Application US/08389487  
 Patent No. 5663291  
 GENERAL INFORMATION:  
 APPLICANT: Obermeier, Ranier  
 APPLICANT: Gerl, Martin  
 APPLICANT: Ludwig, Jurgen

APPLICANT: Sabel, Walter  
TITLE OF INVENTION: Process for Obtaining Insulin Having  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/389,487  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02481.1424-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-389-487-8

Query Match 96.1%; Score 147; DB 1; Length 96;  
Best Local Similarity 96.8%; Pred. No. 2.4e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
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Db 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32  
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RESULT 8  
US-07-800-366-1  
Sequence 1, Application US/07800366  
Patent No. 5250296  
GENERAL INFORMATION:  
APPLICANT: OOTSU, Koichiro  
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/800,366  
FILING DATE: 19911127  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:

NAME: Castle, Donald R  
REGISTRATION NUMBER: 24,220  
REFERENCE/DOCKET NUMBER: 41417(281)  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-3400  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-800-366-1

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
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Db 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
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RESULT 9  
US-08-354-456A-5  
Sequence 5, Application US/08354456A  
Patent No. 5567611  
GENERAL INFORMATION:  
APPLICANT: Ralph, Peter  
APPLICANT: Martin, George  
APPLICANT: Platek, Michael  
APPLICANT: Larrick, James W.  
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding  
TITLE OF INVENTION: Therefor  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: Intellectual Property - R440, P.O. Box 8097  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/354,456A  
FILING DATE: 12-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/995,338  
FILING DATE: 21-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McGarrigle Jr., Phillip L.  
REGISTRATION NUMBER: 31,395  
REFERENCE/DOCKET NUMBER: 750.003/32387  
TELEPHONE: (510) 601-2718  
TELEFAX: (510) 655-3542  
TELEX: n/a  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-456A-5

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31  
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Db 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31

## RESULT 10

US-08-225-224-3  
; Sequence 3, Application US/08225224  
; Patent No. 5635599  
; GENERAL INFORMATION:  
; APPLICANT: PASTAN, Ira  
; APPLICANT: KREITMAN, Robert J.  
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 15280-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown

MOLECULE TYPE: protein  
FEATURE:

NAME/KEY: Protein  
LOCATION: 1..133  
OTHER INFORMATION: /label= IL2  
US-08-225-224-3

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31  
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Db 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31

## RESULT 11

US-08-318-193-89  
; Sequence 89, Application US/08318193  
; Patent No. 5641663  
; GENERAL INFORMATION:

APPLICANT: GARVIN, Robert T.  
APPLICANT: MALEK, Lawrence T.  
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS  
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,193  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,314

FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 18740/116 CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109  
TELEX: 899149

INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-318-193-89

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31  
|||||  
Db 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31

## RESULT 12

US-08-284-393B-1  
; Sequence 1, Application US/08284393B  
; Patent No. 5696234  
; GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.  
APPLICANT: Zurawski, Gerard  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-1

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
|||||  
Db 1 APTSSSTKKTQLQLEHLLLDLQMLINGINNY 31

RESULT 13  
US-08-284-393B-2  
Sequence 2, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
APPLICANT: Zurawski, Gerard  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-2

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
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Db 1 APTSSSTKKTQLQLEHLLLDLQMLINGINNY 31

RESULT 14  
US-08-284-393B-3  
Sequence 3, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
APPLICANT: Zurawski, Gerard  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-3

Query Match 96.1%; Score 147; DB 1; Length 133;  
Best Local Similarity 96.8%; Pred. No. 3.6e-15;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31  
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Db 1 APTSSSTKKTQLQLEHLLLDLQMLINGINNY 31

RESULT 15  
US-08-734-471-1  
Sequence 1, Application US/08734471  
Patent No. 5800810  
GENERAL INFORMATION:  
APPLICANT: Doyle, Michael V.  
APPLICANT: Newell, Arthur D.  
APPLICANT: Nunberg, Jack H.  
APPLICANT: White, Thomas J.  
TITLE OF INVENTION: HUMAN IL-2 AS A VACCINE ADJUVANT  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation, Intellectual Property R440  
STREET: P O Box 8097  
CITY: Emeryville  
STATE: California  
COUNTRY: United States of America  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,471
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,884
; FILING DATE: 24-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 33478/0605.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-734-471-1

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Query Match      96.18; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 APTSSSTKKTKQLQLEHLLKQLQMLINGINNY 31
Db 1 APTSSSTKKTKQLQLEHLLKQLQMLINGINNY 31

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Search completed: February 20, 2003, 10:08:11
Job time : 20.1905 secs

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1	147	96.1	133	9	US-10-051-657A-1	Sequence 1, Appli
2	147	96.1	133	10	US-09-766-543-8	Sequence 8, Appli
3	147	96.1	153	10	US-09-149-721-3	Sequence 3, Appli
4	147	96.1	153	10	US-09-923-246-11	Sequence 11, App
5	147	96.1	381	10	US-09-822-698A-5	Sequence 5, Appli
6	143	93.5	133	10	US-09-766-543-14	Sequence 14, Appl
7	143	93.5	331	10	US-09-033-525-2	Sequence 2, Appli
8	57	37.3	43	10	US-09-835-147-11	Sequence 11, Appl
9	57	37.3	454	10	US-09-835-147-6	Sequence 6, Appli
10	57	37.3	478	10	US-09-835-147-8	Sequence 8, Appli
11	57	37.3	487	10	US-09-835-147-26	Sequence 26, Appl
12	51	33.3	751	10	US-09-881-752A-280	Sequence 280, App
13	51	33.3	866	10	US-09-815-242-11373	Sequence 11373, A
14	50	32.7	37	9	US-10-142-120-1	Sequence 1, Appli
15	47	30.7	226	9	US-09-796-149-5	Sequence 5, Appli
16	47	30.7	256	9	US-10-013-379-25	Sequence 25, Appl
17	47	30.7	515	10	US-09-925-300-1285	Sequence 1285, Ap
18	44	28.8	284	10	US-09-810-997-1	Sequence 1, Appli
19	43.5	28.4	88	10	US-09-864-761-36104	Sequence 36104, A

; PRIOR APPLICATION NUMBER: 60/177,258

OTHER INFORMATION: Description of Artificial Sequence: hIL-2

US-09-766-543-14

Query Match 93.5%; Score 143; DB 10; Length 133;  
Best Local Similarity 96.7%; Pred. No. 1e-14;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 2 PTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 7

US-09-033-525-2  
; Sequence 2, Application US/09033525  
; Patent No. US20020090374A1  
; GENERAL INFORMATION:  
; APPLICANT: Yarkoni, Shai  
; APPLICANT: Ben-Yehudah, Ahmi  
; APPLICANT: Azar, Yehudith  
; APPLICANT: Agellan, Rami  
; APPLICANT: Belostotsky, Ruth  
; APPLICANT: Lorberdoun-Galski, Haya  
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING  
; FILE REFERENCE: 9457-009-999  
; CURRENT APPLICATION NUMBER: US/09/033,525  
; CURRENT FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-033-525-2

Query Match 93.5%; Score 143; DB 10; Length 331;  
Best Local Similarity 96.7%; Pred. No. 3.1e-14;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 4 PTSSSTKKTQLQLEHLLKLQMLNGINNY 33

RESULT 8

US-09-835-147-11  
; Sequence 11, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Mallszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
US-09-835-147-11

; OTHER INFORMATION: construct of human CD39  
US-09-835-147-11

Query Match 37.3%; Score 57; DB 10; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQL 12  
DB 25 APTSSSTKKTQL 36

RESULT 9

US-09-835-147-6  
; Sequence 6, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Mallszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
US-09-835-147-6

Query Match 37.3%; Score 57; DB 10; Length 454;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQL 12  
DB 1 APTSSSTKKTQL 12

RESULT 10

US-09-835-147-8  
; Sequence 8, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Mallszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
US-09-835-147-8

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; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Descriptive
; OTHER INFORMATION: construct
US-09-835-147-8

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Query Match 37.3%; Score 57; DB 10; Length 478;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 12; Conservative 0; Mismatches 0; Indels

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Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 12; Conservative 0; Mismatches 0; Indels

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; TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in t
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-280

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Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
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Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
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Db	624	SESQKDDFIKLGKILKENILNSFNF	651

RESULT 14  
US-10-142-120-1  
; Sequence 1, Application US/10142120  
; Patent No. US20020164302A1  
; GENERAL INFORMATION:  
; APPLICANT: Epstein, Alan L.  
; TITLE OF INVENTION: VASOPERMEABILITY ENHANCING PEPTIDE FRAGMENT OF HUMAN INTERLEUKIN-  
; FILE REFERENCE: 1920-325D2-09801297  
; CURRENT APPLICATION NUMBER: US/10/142,120  
; CURRENT FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 09/443,061  
; PRIOR FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: 08/806,121  
; PRIOR FILING DATE: 1996-12-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-142-120-1

Query Match 32.7%; Score 50; DB 9; Length 37;  
Best Local Similarity 90.0%; Pred. No. 0.3;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 22 OMILINGINNY 31  
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Db 1 EMILINGINNY 10

RESULT 15  
US-09-796-149-5  
; Sequence 5, Application US/09796149  
; Patent No. US20020035079A1  
; GENERAL INFORMATION:  
; APPLICANT: Univ. of Southern California  
; TITLE OF INVENTION: Mutated cyclin G1 protein  
; FILE REFERENCE: 4-31342A/USC  
; CURRENT APPLICATION NUMBER: US/09/796,149  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-149-5

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Best Local Similarity 60.0%; Pred. No. 7.6;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 82 TKKQVLMEHLVLKV 96

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